

having an amino acid sequence of one of SEQ ID NOS: 1 to 2128.

[0608] In specific embodiments, the present invention encompasses an antibody or fragment thereof comprising a VL domain from an scFv having an amino acid sequence of one of SEQ ID NOS: 1 to 2128, wherein said antibody or fragment thereof immunospecifically binds BLYS and which also comprises a VH domain from an scFv having an amino acid sequence of one of SEQ ID NOS: 1 to 2128, and in which said VL and said VH domains are derived from the same scFv having an amino acid sequence of one of SEQ ID NOS: 1 to 2128.

[0609] In specific embodiments, the present invention encompasses an antibody or fragment thereof comprising an amino acid sequence of one of SEQ ID NOS: 2129 to 3227 wherein said antibody or fragment thereof immunospecifically binds BLYS.

[0610] In specific embodiments, the antibody or fragment thereof of the invention is a whole immunoglobulin molecule.

[0611] In specific embodiments, the antibody or fragment thereof of the invention is a Fab fragment.

[0612] In specific embodiments, the antibody or fragment thereof of the invention is a Fv fragment.

[0613] In specific embodiments, the present invention encompasses a chimeric protein comprising the antibody or fragment thereof of the invention covalently linked to a heterologous polypeptide.

[0614] In specific embodiments, the present invention encompasses a composition comprising two or more types of antibodies or fragments or variants thereof, each of which type immunospecifically binds to BLYS, and each of which type of antibody or fragment thereof comprises a VH domain from a different scFv having an amino acid sequence of one of SEQ ID NOS: 1 to 2128.

[0615] In specific embodiments, the present invention encompasses a composition comprising two or more types of antibodies or fragments or variants thereof, each of which type immunospecifically binds to BLYS, and each of which type of antibody or fragment thereof comprises a VL domain from a different scFv having an amino acid sequence of one of SEQ ID NOS: 1 to 2128.

[0616] In specific embodiments, the present invention encompasses a composition comprising two or more types of antibodies or fragments or variants thereof, each of

which type immunospecifically binds to BLYS, and each of which type of antibody or fragment thereof comprises a VL domain from a different scFv having an amino acid sequence of one of SEQ ID NOS: 1 to 2128 and wherein each type of antibody or fragment thereof further comprises a VH domain from a different scFv having an amino acid sequence of one of SEQ ID NOS: 1 to 2128.

[0617] In specific embodiments, the present invention encompasses a composition comprising two or more types of antibodies or fragments or variants thereof, each of which type immunospecifically binds to BLYS, and each of which type of antibody or fragment thereof comprises a VH CDR3 having an amino acid sequence of one of SEQ ID NOS: 3129 to 3227.

[0618] In specific embodiments, the present invention encompasses a panel of two or more types of antibodies or fragments or variants thereof, each of which type immunospecifically binds to BLYS, and each of which type of antibody or fragment thereof comprises a VH domain from a different scFv having an amino acid sequence of one of SEQ ID NO: 1 to 2128.

[0619] In specific embodiments, the present invention encompasses a panel of two or more types of antibodies or fragments or variants thereof, each of which type immunospecifically binds to BLYS, and each of which type of antibody or fragment thereof comprises a VL domain from a different scFv having an amino acid sequence of one of SEQ ID NO: 1 to 2128.

[0620] In specific embodiments, the present invention encompasses a panel of two or more types of antibodies or fragments or variants thereof, each of which type immunospecifically binds to BLYS, and each of which type of antibody or fragment thereof comprises a VL domain from a different scFv having an amino acid sequence of one of SEQ ID NO: 1 to 2128 and wherein each type of antibody or fragment further comprises a VH domain from a different scFv having an amino acid sequence of one of SEQ ID NOS: 1 to 2128.

[0621] In specific embodiments, the present invention encompasses a panel of two or more antibodies or fragments or variants thereof, each of which type immunospecifically binds to BLYS, and each of which type of antibody or fragment thereof comprises a VHCDR3 from a different scFv having an amino acid sequence of one of SEQ ID NOS: 2129 to 3227.

[0622] In specific embodiments, the antibodies or fragments thereof of the antibody panel of the invention, are each in a well of a 96 well plate.

[0623] In specific embodiments, the present invention encompasses an isolated nucleic acid molecule comprising a nucleotide sequence encoding an antibody or fragment thereof comprising a VH domain from an scFv having an amino acid sequence of one of SEQ ID NOS: 1 to 2128, wherein said antibody or fragment thereof immunospecifically binds BLYS.

[0624] In specific embodiments, the present invention encompasses an isolated nucleic acid molecule comprising a nucleotide sequence encoding an antibody or fragment thereof comprising a VH domain from an scFv having an amino acid sequence of one of SEQ ID NOS: 1 to 46, 321 to 329, 1563 to 1595, and 1881 to 1908, wherein said antibody or fragment thereof immunospecifically binds BLYS.

[0625] In specific embodiments, the present invention encompasses an isolated nucleic acid molecule comprising a nucleotide sequence encoding an antibody or fragment thereof comprising a VH domain from an scFv having an amino acid sequence of one of SEQ ID NOS: 1881 to 1908, wherein the antibody or fragment thereof immunospecifically binds the membrane-bound form of BLYS.

[0626] In specific embodiments, the present invention encompasses an isolated nucleic acid molecule comprising a nucleotide sequence encoding an antibody or fragment thereof comprising a VH domain from an scFv having an amino acid sequence of one of SEQ ID NOS: 1563 to 1569, wherein said antibody or fragment thereof immunospecifically binds the soluble form of BlyS. The present invention also encompasses vectors comprising the isolated nucleic acid molecule described above, including vectors comprising a nucleotide sequence which regulates the expression of the antibody or fragment thereof encoded by the above-described nucleic acid molecule. Additionally the present invention also encompasses host cells, including mammalian host cells, comprising the above-described nucleic acid molecule which is operably linked to a heterologous promoter, as well as host cells, including mammalian host cells, comprising the above-described vectors. Additionally, the present invention also provides a method for producing an antibody or fragment thereof comprising culturing the above-described host cells under conditions in which the nucleic acid molecule is expressed.

[0627] In specific embodiments, the present invention encompasses an isolated

nucleic acid molecule comprising a nucleotide sequence encoding an antibody or fragment thereof comprising a VL domain from an scFv having an amino acid sequence of one of SEQ ID NOS: 1 to 2128, wherein said antibody or fragment thereof immunospecifically binds BLYS. The present invention also encompasses vectors comprising the isolated nucleic acid molecule described above, including vectors comprising a nucleotide sequence which regulates the expression of the antibody or fragment thereof encoded by the above-described nucleic acid molecule. Additionally the present invention also encompasses host cells, including mammalian host cells, comprising the above-described nucleic acid molecule which is operably linked to a heterologous promoter, as well as host cells, including mammalian host cells, comprising the above-described vectors. Additionally, the present invention also provides a method for producing an antibody or fragment thereof comprising culturing the above-described host cells under conditions in which the nucleic acid molecule is expressed.

[0628] In specific embodiments, the present invention encompasses an isolated nucleic acid molecule comprising a nucleotide sequence encoding an antibody or fragment thereof comprising a VL domain from an scFv having an amino acid sequence of one of SEQ ID NOS: 1 to 46, 321 to 329, 1563 to 1595, and 1881 to 1908, wherein said antibody or fragment thereof immunospecifically binds BLYS. The present invention also encompasses vectors comprising the isolated nucleic acid molecule described above, including vectors comprising a nucleotide sequence which regulates the expression of the antibody or fragment thereof encoded by the above-described nucleic acid molecule. Additionally the present invention also encompasses host cells, including mammalian host cells, comprising the above-described nucleic acid molecule which is operably linked to a heterologous promoter, as well as host cells, including mammalian host cells, comprising the above-described vectors. Additionally, the present invention also provides a method for producing an antibody or fragment thereof comprising culturing the above-described host cells under conditions in which the nucleic acid molecule is expressed.

[0629] In specific embodiments, the present invention encompasses an isolated nucleic acid molecule comprising a nucleotide sequence encoding an antibody or fragment thereof comprising a VL domain from an scFv having an amino acid sequence of one of SEQ ID NOS: 1881 to 2128, wherein the antibody or fragment thereof immunospecifically binds the membrane-bound form of BLYS. The present invention also

encompasses vectors comprising the isolated nucleic acid molecule described above, including vectors comprising a nucleotide sequence which regulates the expression of the antibody or fragment thereof encoded by the above-described nucleic acid molecule. Additionally the present invention also encompasses host cells, including mammalian host cells, comprising the above-described nucleic acid molecule which is operably linked to a heterologous promoter, as well as host cells, including mammalian host cells, comprising the above-described vectors. Additionally, the present invention also provides a method for producing an antibody or fragment thereof comprising culturing the above-described host cells under conditions in which the nucleic acid molecule is expressed.

[0630] In specific embodiments, the present invention encompasses an isolated nucleic acid molecule comprising a nucleotide sequence encoding an antibody or fragment thereof comprising a VL domain from an scFv having an amino acid sequence of one of SEQ ID NOS: 1563 to 1880, wherein said antibody or fragment thereof immunospecifically binds the soluble form of BlyS. The present invention also encompasses vectors comprising the isolated nucleic acid molecule described above, including vectors comprising a nucleotide sequence which regulates the expression of the antibody or fragment thereof encoded by the above-described nucleic acid molecule. Additionally the present invention also encompasses host cells, including mammalian host cells, comprising the above-described nucleic acid molecule which is operably linked to a heterologous promoter, as well as host cells, including mammalian host cells, comprising the above-described vectors. Additionally, the present invention also provides a method for producing an antibody or fragment thereof comprising culturing the above-described host cells under conditions in which the nucleic acid molecule is expressed.

[0631] In specific embodiments, the present invention encompasses an isolated nucleic acid molecule comprising a nucleotide sequence encoding an antibody or fragment thereof comprising a VL domain from an scFv having an amino acid sequence of one of SEQ ID NOS: 1 to 2128, wherein said antibody or fragment thereof immunospecifically binds BlyS and which also comprises a VH domain from an scFv having an amino acid sequence of one of SEQ ID NOS: 1 to 2128. The present invention also encompasses vectors comprising the isolated nucleic acid molecule described above, including vectors comprising a nucleotide sequence which regulates the expression of the antibody or fragment thereof encoded by the above-described nucleic acid molecule. Additionally the

present invention also encompasses host cells, including mammalian host cells, comprising the above-described nucleic acid molecule which is operably linked to a heterologous promoter, as well as host cells, including mammalian host cells, comprising the above-described vectors. Additionally, the present invention also provides a method for producing an antibody or fragment thereof comprising culturing the above-described host cells under conditions in which the nucleic acid molecule is expressed.

[0632] In specific embodiments, the present invention encompasses an isolated nucleic acid molecule comprising a nucleotide sequence encoding an antibody or fragment thereof comprising a VL domain from an scFv having an amino acid sequence of one of SEQ ID NOS: 1 to 2128, wherein said antibody or fragment thereof immunospecifically binds BLYS and which also comprises a VH domain from an scFv having an amino acid sequence of one of SEQ ID NOS: 1 to 2128 and in which said VL domain and said VH domain are derived from the same scFv having an amino acid sequence of one of SEQ ID NOS: 1 to 2128. The present invention also encompasses vectors comprising the isolated nucleic acid molecule described above, including vectors comprising a nucleotide sequence which regulates the expression of the antibody or fragment thereof encoded by the above-described nucleic acid molecule. Additionally the present invention also encompasses host cells, including mammalian host cells, comprising the above-described nucleic acid molecule which is operably linked to a heterologous promoter, as well as host cells, including mammalian host cells, comprising the above-described vectors. Additionally, the present invention also provides a method for producing an antibody or fragment thereof comprising culturing the above-described host cells under conditions in which the nucleic acid molecule is expressed.

[0633] In specific embodiments, the present invention encompasses an isolated nucleic acid molecule comprising a nucleotide sequence encoding an antibody or fragment thereof comprising a VHCDR3 from an scFv having an amino acid sequence of one of SEQ ID NOS: 2129 to 3227, wherein said antibody or fragment thereof immunospecifically binds BLYS. The present invention also encompasses vectors comprising the isolated nucleic acid molecule described above, including vectors comprising a nucleotide sequence which regulates the expression of the antibody or fragment thereof encoded by the above-described nucleic acid molecule. Additionally the present invention also encompasses host cells, including mammalian host cells,

comprising the above-described nucleic acid molecule which is operably linked to a heterologous promoter, as well as host cells, including mammalian host cells, comprising the above-described vectors. Additionally, the present invention also provides a method for producing an antibody or fragment thereof comprising culturing the above-described host cells under conditions in which the nucleic acid molecule is expressed.

[0634] In specific embodiments, the present invention provides an antibody or fragment thereof that immunospecifically binds to BLYS, said antibody or fragment thereof comprising an amino acid sequence of a VH domain encoded by a nucleotide sequence that hybridizes under stringent conditions to a nucleotide sequence encoding a VH domain from an scFv having an amino acid sequence of one of SEQ ID NOS: 1 to 2128.

[0635] In specific embodiments, the present invention provides an antibody or fragment thereof that immunospecifically binds to BLYS, said antibody or fragment thereof comprising an amino acid sequence of a VL domain encoded by a nucleotide sequence that hybridizes under stringent conditions to a nucleotide sequence encoding a VL domain from an scFv having an amino acid sequence of one of SEQ ID NOS: 1 to 2128.

[0636] In specific embodiments, the present invention provides an antibody or fragment thereof that immunospecifically binds to BLYS, said antibody or fragment thereof comprising an amino acid sequence of a VH domain encoded by a nucleotide sequence that hybridizes under highly stringent conditions to a nucleotide sequence encoding a VH domain from an scFv having an amino acid sequence of one of SEQ ID NOS: 1 to 2128.

[0637] In specific embodiments, the present invention provides an antibody or fragment thereof that immunospecifically binds to BLYS, said antibody or fragment thereof comprising an amino acid sequence of a VL domain encoded by a nucleotide sequence that hybridizes under highly stringent conditions to a nucleotide sequence encoding a VL domain from an scFv having an amino acid sequence of one of SEQ ID NOS: 1 to 2128.

[0638] In specific embodiments, the present invention provides an antibody or fragment thereof that immunospecifically binds to BLYS, said antibody or fragment thereof comprising an amino acid sequence of a CDR encoded by a nucleotide sequence

that hybridizes under stringent conditions to a nucleotide sequence encoding a CDR from an scFv having an amino acid sequence of one of SEQ ID NOS: 1 to 2128.

[0639] In specific embodiments, the present invention provides an antibody or fragment thereof that immunospecifically binds to BLYS, said antibody or fragment thereof comprising an amino acid sequence of a CDR encoded by a nucleotide sequence that hybridizes under highly stringent conditions to a nucleotide sequence encoding a CDR from an scFv having an amino acid sequence of one of SEQ ID NOS: 1 to 2128.

[0640] In specific embodiments, the present invention provides an antibody or fragment thereof that immunospecifically binds to BLYS, said antibody or fragment thereof comprising an amino acid sequence of a VH CDR3 encoded by a nucleotide sequence that hybridizes under stringent conditions to a nucleotide sequence encoding a VH CDR3 having an amino acid sequence of one of SEQ ID NOS: 2129 to 3227.

[0641] In specific embodiments, the present invention provides an antibody or fragment thereof that immunospecifically binds to BLYS, said antibody or fragment thereof comprising an amino acid sequence of a VH CDR3 encoded by a nucleotide sequence that hybridizes under highly stringent conditions to a nucleotide sequence encoding a VH CDR3 having an amino acid sequence of one of SEQ ID NOS: 2129 to 3227.

[0642] In specific embodiments, the present invention provides a method for detecting of aberrant expression of BLYS, comprising:

[0643] assaying the level of BLYS expression in cells or a tissue sample of an individual using one or more antibodies or fragments or variants thereof that immunospecifically bind BLYS; and

[0644] comparing the level of BLYS assayed in the cells or a tissue sample with a standard level of BLYS or a level of BLYS in cells or a tissue sample from an individual without aberrant BLYS expression, wherein an increase or decrease in the assayed level of BLYS or level in cells or a tissue sample from an individual without aberrant BLYS expression compared to the standard level of BLYS is indicative of aberrant expression.

[0645] In specific embodiments, the present invention provides a method for diagnosing a disease or disorder associated with aberrant BLYS expression or activity, comprising:

[0646] administering to a subject an effective amount of a labeled antibody or

fragment thereof that immunospecifically binds to BLyS;

[0647] waiting for a time interval following the administering for permitting the labeled antibody or fragment thereof to preferentially concentrate at sites in the subject where BLyS is expressed;

[0648] determining background level; and

[0649] detecting the labeled antibody or fragment thereof in the subject, such that detection of labeled antibody or fragment thereof above the background level indicates that the subject has a particular disease or disorder associated with aberrant expression of BLyS.

[0650] In specific embodiments, the antibody or fragment thereof utilized in the two methods described immediately above comprises a VH domain from an scFv having an amino acid sequence of one of SEQ ID NOS: 1 to 2128.

[0651] In specific embodiments, the antibody or fragment thereof utilized in the two methods described immediately above comprises a VL domain from an scFv having an amino acid sequence of one of SEQ ID NOS: 1 to 2128.

[0652] In specific embodiments, the antibody or fragment thereof utilized in the two methods described immediately above comprises a VH CDR3 having an amino acid sequence of one of SEQ ID NOS: 2129 to 3227.

[0653] In specific embodiments, the antibody or fragment thereof utilized in the two methods described immediately above is conjugated to a diagnostic agent.

[0654] In specific embodiments, the antibody or fragment thereof utilized in the two methods described immediately above is conjugated to a diagnostic agent wherein the diagnostic agent is horseradish peroxidase, alkaline phosphatase, beta-galactosidase, or acetylcholinesterase.

[0655] In specific embodiments, the antibody or fragment thereof utilized in the two methods described immediately above is conjugated to a diagnostic agent wherein the diagnostic agent is fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin.

[0656] In specific embodiments, the antibody or fragment thereof utilized in the two methods described immediately above is conjugated to a diagnostic agent wherein the diagnostic agent is ^{125}I , ^{131}I , ^{111}In , ^{90}Y or ^{99}Tc .

[0657] In specific embodiments, the antibody or fragment thereof utilized in the

two methods described immediately above is conjugated to a diagnostic agent wherein the diagnostic agent is luciferase, luciferin or aequorin.

[0658] A pharmaceutical composition comprising at least one antibody or fragment thereof of comprising a VH domain from an scFv having an amino acid sequence of one of SEQ ID NOS: 1 to 2128, wherein said antibody or fragment thereof immunospecifically binds BLYS and a pharmaceutically acceptable carrier.

[0659] A pharmaceutical composition comprising at least one antibody or fragment thereof of comprising a VL domain from an scFv having an amino acid sequence of one of SEQ ID NOS: 1 to 2128, wherein said antibody or fragment thereof immunospecifically binds BLYS and a pharmaceutically acceptable carrier.

[0660] A pharmaceutical composition comprising at least one antibody or fragment thereof of comprising a VL domain from an scFv having an amino acid sequence of one of SEQ ID NOS: 1 to 2128, wherein said antibody or fragment thereof immunospecifically binds BLYS and which also comprises a VH domain from an scFv having an amino acid sequence of one of SEQ ID NOS: 1 to 2128 and a pharmaceutically acceptable carrier.

[0661] A pharmaceutical composition comprising at least one antibody or fragment thereof of comprising an amino acid sequence of one of SEQ ID NOS: 2129 to 3227 wherein said antibody or fragment thereof immunospecifically binds BLYS and a pharmaceutically acceptable carrier.

[0662] A method of treating, preventing or ameliorating a disease or disorder associated with aberrant BLYS expression or activity, comprising administering to an animal in need thereof the pharmaceutical composition comprising at least one antibody or fragment thereof of comprising a VL domain from an scFv having an amino acid sequence of one of SEQ ID NOS: 1 to 2128, wherein said antibody or fragment thereof immunospecifically binds BLYS and which also comprises a VH domain from an scFv having an amino acid sequence of one of SEQ ID NOS: 1 to 2128 and a pharmaceutically acceptable carrier in an amount effective to treat, prevent or ameliorate the disease or disorder. This method may be used to treat an infectious disorder, cancer, and/or an autoimmune disease such as lupus or glomerular nephritis.

[0663] A method of treating, preventing or ameliorating a disease or disorder associated with aberrant BLYS expression or activity, comprising administering to an

animal in need thereof the pharmaceutical composition comprising at least one antibody or fragment thereof of comprising a VL domain from an scFv having an amino acid sequence of one of SEQ ID NOS: 1 to 2128, wherein said antibody or fragment thereof immunospecifically binds BLYS and a pharmaceutically acceptable carrier in an amount effective to treat, prevent or ameliorate the disease or disorder. This method may be used to treat an infectious disorder, cancer, and/or an autoimmune disease such as lupus or glomerular nephritis.

[0664] A method of treating, preventing or ameliorating a disease or disorder associated with aberrant BLYS expression or activity, comprising administering to an animal in need thereof the pharmaceutical composition comprising at least one antibody or fragment thereof of comprising a VL domain from an scFv having an amino acid sequence of one of SEQ ID NOS: 1 to 2128, wherein said antibody or fragment thereof immunospecifically binds BLYS and which also comprises a VH domain from an scFv having an amino acid sequence of one of SEQ ID NOS: 1 to 2128 and a pharmaceutically acceptable carrier in an amount effective to treat, prevent or ameliorate the disease or disorder. This method may be used to treat an infectious disorder, cancer, and/or an autoimmune disease such as lupus or glomerular nephritis.

[0665] A method of treating, preventing or ameliorating a disease or disorder associated with aberrant BLYS expression or activity, comprising administering to an animal in need thereof the pharmaceutical composition of comprising at least one antibody or fragment thereof of comprising an amino acid sequence of one of SEQ ID NOS: 2129 to 3227 wherein said antibody or fragment thereof immunospecifically binds BLYS and a pharmaceutically acceptable carrier in an amount effective to treat, prevent or ameliorate the disease or disorder. This method may be used to treat an infectious disorder, cancer, and/or an autoimmune disease such as lupus or glomerular nephritis.

[0666] This method may be used to treat an infectious disorder, cancer, and/or an autoimmune disease such as lupus or glomerular nephritis.

EXAMPLES

Abbreviations

0.2 M Tris-HCl, 0.5 mM EDTA, 0.5 M sucrose (TES)

1-ethyl-3-[3-dimethylaminopropyl]carbo diimide hydrochloride (EDC)

2TY supplemented with 100µg/ml ampicillin and 2% glucose (2TYAG)

2TY supplemented with 100µg/ml ampicillin and 50µg/ml kanamycin (2TYAK)

3,3',5,5'-Tetramethyl Benzidine (TMB)

50% inhibitory concentration (IC₅₀)

6xPBS containing 18% Marvel blocking solution (6xMPBS)

Absorbance (A)

Bovine serum albumin (BSA)

Enzyme linked immunosorbent assay (ELISA)

Foetal calf serum (FCS)

Heavy chain variable (V_H)

Hepes buffered saline (HBS)

Horseradish peroxidase (HRP)

Immobilised Metal Affinity Chromatography (IMAC)

Isopropyl β-D-thiogalactopyranoside (IPTG)

Light chain variable(V_L)

Multiplicity of infection (MOI)

N-[2-hydroxyethyl]piperazine-N'-[2-ethanesulfonic acid] (Hepes)

Nanomolar (nM)

N-Hydroxysuccinimide (NHS)

PBS containing 3% Marvel (MPBS)

Phosphate Buffered Saline (PBS)

Phosphate Buffered Saline + 0.1% (v/v) Tween 20 (PBST)

Picomolar (pM)

Single chain fragment variable (scFv)

Tumour Necrosis Factor-alpha (TNF-α)

Tumour Necrosis Factor-beta (TNF-β)

TNF-related apoptosis inducing ligand (TRAIL)

Definitions:

[0667] In the following section “immobilized BLyS” refers to a soluble form of BLyS or biotinylated BLyS coated on a plastic assay plate (e.g., a 96 well plate), but does not refer to histidine tagged BLyS coated on a plastic assay plate.; “biotinylated BLyS” is a soluble form of BLyS except when used to coat an ELISA plate, in which case it would be “immobilized BLyS.” Membrane bound forms of BLyS include, but are not limited to, U937 and P388 plasma membranes.

Example 1: Antibodies Immunospecifically Binding to Soluble And Membrane-Bound BLyS

[0668] A library of phage was screened in an assay to identify those phage displaying scFvs that immunospecifically bind to the soluble and membrane-bound forms of BLyS. Phage displaying scFvs that bound to immobilized BLyS were identified after panning on immobilized BLyS and assessment by ELISA for binding to immobilized BLyS. The BLyS that was immobilized on plates for these assays was purified from supernatants of Sf9 cells infected with a baculovirus expression construct as described in Moore et al., Science 285:260-263 which is hereby incorporated by reference in its entirety. Each of the identified scFvs were then sequenced. Certain sequences were isolated multiple times, thus a panel (panel 1) containing one member of each unique sequences was generated and further characterized for their ability to immunospecifically bind to the soluble and membrane-bound forms of BLyS.

[0669] The derived amino acid sequences of these scFvs are shown in Table 1 above. The individual V_H and V_L segments of the scFvs were aligned to the known human germline sequences in V-BASE (Tomlinson et al, www.mrc-cpe.cam.ac.uk) and the closest germline identified.

Example 2: Specificity of scFvs for BLyS and Membrane-Bound BLyS

[0670] The specificity of each of the scFvs for both BLyS and membrane-bound BLyS was determined by phage ELISA. BLyS was immobilised onto plastic as a purified soluble form of the protein or as a membrane-bound form present on plasma membrane preparations from the human macrophage-like cell line, U937.

Maintenance of U937 Cells

[0671] U937 cells are a human monocyte-like, histiocytic lymphoma cell line known to express BLYS on their plasma membranes. They were maintained in RPMI-1640 supplemented with 4mM L-glutamine, 10% FCS, 10 U penicillin, 100 g/ml streptomycin (all reagents from Sigma). The cells were thawed from frozen stock and are either used for plasma membrane preparation, or split 1:5, after 2 days in culture when the cell density reaches $1 \times 10^6/\text{ml}$.

Preparation of U937 Plasma Membranes

[0672] To prepare plasma membranes, 1×10^9 U937 cells were harvested from their culture medium by centrifugation at 1000 rpm at 4°C for 5 minutes in a benchtop centrifuge. The cells were resuspended in 40 ml 12 mM Tris, pH 7.5, 250 mM sucrose and placed on ice. The cells are then lysed using a hand-held electric homogenizer (Labortechnik IKA Ultra-Turrax) for four, one minute, bursts. To check that cell lysis had occurred, 10 μl cell lysate was added to 10 μl Trypan blue and the cell lysate was examined under a microscope. After confirming lysis, the homogenate was centrifuged at $270 \times g$, for 10 minutes at 4°C to pellet the nuclear fraction and the supernatant was retained. The supernatant was centrifuged at $8000 \times g$, 10 mins, 4°C, to pellet the mitochondrial and lysosomal fractions and the supernatant was retained. The supernatant was then centrifuged at $100000 \times g$, 60 mins, 4°C to pellet the plasma membrane enriched fraction. The supernatant was discarded and the plasma membrane pellet was resuspended in 1 ml PBS and stored at -70°C. The protein concentration of the plasma membrane fraction was determined using a protein quantification kit (Biorad). Typical yields were between 5 and 10 mg of plasma membranes.

Phage ELISA

[0673] To determine the specificity of each of the unique scFvs, a phage ELISA was performed for each scFv against human BLYS, U937 plasma membranes, TNF α (R&D Systems, Minneapolis, MN), BSA and uncoated well. Individual *E. coli* colonies containing a phagemid representing one of the unique scFvs from panel 1 were inoculated into 96-well plates containing 100 μl 2TYAG medium per well. Plates were incubated at 37°C for 4 hours, shaking. M13KO7 helper phage was added to each well to a MOI of 10

and the plates were incubated for a further 1 hour at 37°C. The plates were centrifuged in a benchtop centrifuge at 2000 rpm for 10 minutes. The supernatant was removed and cell pellets were resuspended in 100 µl 2TYAK and incubated at 30°C overnight, shaking. The next day, plates were centrifuged at 2000 rpm for 10 min and the 100 µl phage-containing supernatant from each well carefully transferred into a fresh 96-well plate. Twenty µl of 6xMPBS was added to each well, and incubated at room temperature for 1 hour to pre-block the phage prior to ELISA.

[0674] Flexible 96-well plates (Falcon) were coated overnight at 4°C with human BLyS (1 µg/ml) in PBS, U937 plasma membranes (10 µg/ml) in PBS, TNFα (1 µg/ml) in PBS, BSA (1 µg/ml) in PBS, or PBS. After coating, the solutions were removed from the wells, and the plates were blocked for 1 hour at room temperature in MPBS. The plates were washed 3 times with PBS and then 50 µl of pre-blocked phage was added to each well. The plates were incubated at room temperature for 1 hour and then washed with 3 changes of PBST followed by 3 changes of PBS. To each well, 50 µl of an anti-gene VIII-HRP conjugate (Pharmacia) at a 1 to 5000 dilution in MPBS was added and the plates incubated at room temperature for 1 hour. Each plate was washed three times with PBST followed by three times with PBS. Then 50 µl of an HRP-labelled anti-mouse polymer (DAKO EnVision) diluted 1/50 in 3% MPBS was added and incubated for 1 hour at room temperature. Each plate was then washed three times with PBST followed by three times with PBS. Fifty µl of TMB substrate was then added to each well, and incubated at room temperature for 30 minutes or until colour development. The reaction was stopped by the addition of 25 µl of 0.5 M H₂SO₄. The signal generated was measured by reading the absorbance at 450nm (A₄₅₀) using a microtiter plate reader (Bio-Rad 3550).

[0675] The results for 3 clones (I006E07, I008D05 and I016F04) are shown in Figure 1. All 3 scFvs recognize immobilized BLyS and U937 plasma membranes but do not recognize TNFα, BSA or an uncoated well (PBS only). These results indicate that these scFvs specifically recognize immobilized BLyS and membrane-bound BLyS.

Example 3: Inhibition in an *In Vitro* Receptor Binding Assay by Phage ScFvs

[0676] All of the unique phage scFvs in panel 1 were assessed for their ability to inhibit soluble BLyS binding to its cognate receptor on IM9 cells.

Biotinylation of BLYS

[0677] One hundred μg of either human or mouse BLYS was dialysed overnight at 4°C against 50 mM sodium bicarbonate (sodium hydrogen carbonate) pH8.5 using a slide-a-lyzer cassette (Pierce). The next day, NHS-biotin (Pierce) was dissolved in DMSO to 13.3 mg/ml. This was then added to the BLYS at a molar ratio of 20:1 biotin:BLYS, mixed and incubated on ice for 2 hours. The biotinylated BLYS was then dialysed back into sterile PBS (Sigma) using a slide-a-lyzer cassette overnight at 4°C . The biological activity of the biotinylated BLYS was confirmed using the receptor binding inhibition assay (see below).

Maintenance of IM9 cells

[0678] IM9 cells are a human B lymphocyte cell line. They were maintained in RPMI-1640 supplemented with 4 mM L-glutamine, 10% FCS, 10 U penicillin, 100 g/ml streptomycin (all reagents from Sigma). The cells are thawed from frozen stock and can be used in assays after 5 days in culture when they reach a density of $4 - 8 \times 10^5$ /ml.

Receptor binding inhibition assay

[0679] Individual *E. coli* colonies containing a phagemid representing one of the unique scFvs from panel 1 were inoculated into 96-well plates containing 100 μl 2TYAG medium per well. Plates were incubated at 37°C for 4 hours, shaking. M13KO7 helper phage was added to each well to a MOI of 10 and the plates were incubated for a further 1 hour at 37°C . The plates were centrifuged in a benchtop centrifuge at 2000 rpm for 10 minutes. The supernatant was removed and cell pellets were resuspended in 100 μl 2TYAK and incubated at 30°C overnight, shaking. The next day, plates were centrifuged at 2000 rpm for 10 min and the 100 μl phage-containing supernatant from each well carefully transferred into a fresh 96-well plate. Phage were diluted 1 in 2 in MPBS prior to use.

[0680] Flat-bottomed 96-well plates (Costar) were coated with 100 μl per well of a 1:10 dilution of poly-L-lysine (Sigma) in PBS for 1 hour at room temperature. The plates were then washed twice with water, allowed to air-dry and placed at 4°C overnight. One hundred μl of IM9 cells (at 10^6 /ml in RPMI-1640 culture medium) were then added to each well. Plates were then centrifuged at 3200 rpm for 5 mins to pellet the cells. The

media was carefully aspirated and 200 μ l of MPBS added to each well. The plates were then allowed to block for 1 hour at room temperature.

[0681] To a separate 96-well plate 10 μ l of biotinylated BLYS (at 162.5 ng/ml) in MPBS was added to each well to give a final concentration of 25 ng/ml. Fifty-five μ l of each appropriate phage supernatant was added to each well and the final volume in each well was 65 μ l. Plates were then incubated at room temperature for 30 minutes.

[0682] The IM9 coated plates were washed twice in PBS, tapped dry and immediately 50 μ l of the phage/biotinylated-BLYS mix was added and incubated at room temperature for 1 hour. Plates were washed three times in PBST and three times in PBS, tapped dry and 50 μ l of streptavidin-Delfia (Wallac) was added to each well at 1:1000 dilution in the Manufacturer's assay buffer. The plates were then incubated at room temperature for 1 hour and washed six times in Delfia wash solution (Wallac). After tapping the plates dry, 100 μ l per well of Delfia enhancement solution (Wallac) was added. The plates were gently tapped to encourage micelle formation, incubated at room temperature for 10 minutes, and fluorescence read on a Wallac 1420 workstation at 6520 nM.

[0683] Results for 3 phage scFvs (I001C09, I018D07 and I016H07) that inhibited the binding of biotinylated BLYS are shown in Figure 2. Maximal binding of biotinylated BLYS to its receptor (bio-BLYS only), the background signal in the absence of biotinylated BLYS (no bio-BLYS), and results with an irrelevant (*i.e.*, does not recognize BLYS) phage antibody are also shown. All 3 phage scFvs inhibited biotinylated BLYS binding to its receptor on IM9 cells, identifying these scFvs as scFvs that bind the soluble form of BLYS. These scFvs also bind to U937 membranes, thus they also bind the membrane bound form of BLYS.

[0684] Forty-eight of the scFvs from panel 1 that demonstrated the greatest inhibition as phage particles in this assay were chosen for further study. These 48 scFvs are listed in Table 3.

Table 3. scFvs that Inhibit the Binding of Biotinylated-BLYS to its Receptor

Antibody	Antibody	Antibody	Antibody	Antibody
----------	----------	----------	----------	----------

I008C02	I029D07	I008C03	I008C12	I028A06
I022E02	I061E07	I007H08	I061H01	I031C03
I018C02	I006D07	I008A11	I006D08	I031F02
I008B01	I017D10	I061D02	I026E03	I031F09
I016F04	I007B03	I008A09	I027A07	I031G11
I016E05	I018C10	I007F11	I016H07	I050A07
I018H08	I001C09	I037E07	I021B05	I050A12
I018H09	I018D07	I037E12	I031G10	I050B11
	I029F11	I016F02	I031G08	I051C04
	I022D01		I031C07	I003F12
			I012A06	

Example 4: Specificity of Anti-BLyS Antibodies

[0685] The specificity of the 48 scFvs listed in Table 3 for human and murine BLyS was determined using phage ELISA.

Phage ELISA

[0686] To determine the specificity of the 48 scFvs, a phage ELISA was performed against human and mouse BLyS, and a panel of related and unrelated human antigens: Fas ligand, TRAIL, TNF α , TNF β , and PBS. The : Fas ligand, TRAIL, TNF α , and TNF β antigens were obtained from R&D Systems, Minneapolis, MN. Individual *E. coli* colonies containing phagemid were inoculated into 5 ml 2YTAG and incubated at 37°C for 4 hours, shaking. M13KO7 helper phage (Pharmacia) was added to each tube to a MOI of 10 and incubated for 30 minutes at 37°C for 1 hour, the first 30 minutes static and the final 30 minutes with gentle shaking. Cells were pelleted by centrifugation at 3,500 rpm for 10 minutes and the supernatant discarded. Cell pellets were resuspended in 5 ml 2TYAK and incubated at 30°C overnight with shaking. The next day, the cells were pelleted by centrifugation at 3,500 rpm for 10 minutes. The phage-containing supernatant (5 ml) was carefully transferred to a fresh tube, 1 ml of 6MPBS was added, and the tube was incubated at room temperature for 1 hour to pre-block the phage prior to ELISA.

[0687] All antigens were coated at 1 µg/ml. ELISAs were performed essentially as described in Example 2. The only exception to this being the detection of phage antibody binding to mouse BLyS where the step involving incubation with the HRP-labelled anti-mouse polymer was omitted. Binding to mouse BLyS was detected with TMB as in Section Example 2.

[0688] All 48 scFvs are specific for immobilized human BLyS and 43 out of the 48 scFvs cross-react with immobilized mouse BLyS but not with any other unrelated or related antigen tested. I008C03, I007F11, I037E07, I037E12, and I016H07 did not bind murine BLyS. Results for two scFvs, I022D01 and I031F02, are shown in Figure 3. Both these scFvs specifically recognize human and mouse BLyS but not any other unrelated or related antigen tested.

Example 5: Specificity for the Membrane-Bound Form of BLyS

[0689] The specificity of 48 scFvs for membrane-bound BLyS was determined by the phage ELISA described in Example 2. BLyS was immobilised onto plastic as a membrane-bound form present on plasma membranes preparations from the human macrophage-like cell line, U937. This cell line is known to express the membrane-bound form of human BLyS.

[0690] To demonstrate that this binding is specific for membrane-bound BLyS, a competition ELISA was developed to determine if the ELISA signal for an individual antibody on U937's could be competed out by pre-incubation with either BLyS or TNFα. An anti-BLyS antibody that also recognizes membrane-bound BLyS would be expected to demonstrate a signal reduction with free BLyS but not free TNFα.

Competition ELISA

[0691] Individual *E. coli* colonies containing phagemid for each of the 48 scFvs listed in Table 3 were inoculated into 5 ml 2YTAG and incubated at 37°C for 4 hours, shaking. M13KO7 helper phage (Pharmacia) was added to each tube to a MOI of 10 and incubated for 30 minutes at 37° C for 1 hour, the first 30 minutes static and the final 30 minutes with gentle shaking. Cells were pelleted by centrifugation at 3,500 rpm for 10

[0687] All antigens were coated at 1 µg/ml. ELISAs were performed essentially as described in Example 2. The only exception to this being the detection of phage antibody binding to mouse BLyS where the step involving incubation with the HRP-labelled anti-mouse polymer was omitted. Binding to mouse BLyS was detected with TMB as in Section Example 2.

[0688] All 48 scFvs are specific for immobilized human BLyS and 43 out of the 48 scFvs cross-react with immobilized mouse BLyS but not with any other unrelated or related antigen tested. I008C03, I007F11, I037E07, I037E12, and I016H07 did not bind murine BLyS. Results for two scFvs, I022D01 and I031F02, are shown in Figure 3. Both these scFvs specifically recognize human and mouse BLyS but not any other unrelated or related antigen tested.

Example 5: Specificity for the Membrane-Bound Form of BLyS

[0689] The specificity of 48 scFvs for membrane-bound BLyS was determined by the phage ELISA described in Example 2. BLyS was immobilised onto plastic as a membrane-bound form present on plasma membranes preparations from the human macrophage-like cell line, U937. This cell line is known to express the membrane-bound form of human BLyS.

[0690] To demonstrate that this binding is specific for membrane-bound BLyS, a competition ELISA was developed to determine if the ELISA signal for an individual antibody on U937's could be competed out by pre-incubation with either BLyS or TNFα. An anti-BLyS antibody that also recognizes membrane-bound BLyS would be expected to demonstrate a signal reduction with free BLyS but not free TNFα.

Competition ELISA

[0691] Individual *E. coli* colonies containing phagemid for each of the 48 scFvs listed in Table 3 were inoculated into 5 ml 2YTAG and incubated at 37°C for 4 hours, shaking. M13KO7 helper phage (Pharmacia) was added to each tube to a MOI of 10 and incubated for 30 minutes at 37° C for 1 hour, the first 30 minutes static and the final 30 minutes with gentle shaking. Cells were pelleted by centrifugation at 3,500 rpm for 10 minutes and the supernatant discarded. Cell pellets were resuspended in 5 ml 2TYAK and incubated at 30°C overnight with shaking. The next day, the cells were pelleted by

<211> 251
 <212> PRT
 <213> Homo sapiens

<400> 14

Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His
 20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
 35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Pro Phe Tyr Asp Thr Leu Thr Arg Tyr Val Phe Gln Val Trp
 100 105 110

Val Ala Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr
 130 135 140

Thr Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Glu Arg
 145 150 155 160

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val
 165 170 175

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr
 180 185 190

Gly Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser
 195 200 205

Glu Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
 210 215 220

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr
 225 230 235 240

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
 245 250

<210> 15
 <211> 251
 <212> PRT
 <213> Homo sapiens

<400> 15
 Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His
 20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
 35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Pro Phe Tyr Asp Thr Leu Thr Gly Tyr Val Phe Gln Val Trp
 100 105 110

Val Ala Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr
 130 135 140

Thr Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Glu Arg
 145 150 155 160

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val
 165 170 175

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr
180 185 190

Gly Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

Glu Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
210 215 220

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr
225 230 235 240

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
245 250

<210> 16
<211> 251
<212> PRT
<213> Homo sapiens

<400> 16
Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Pro Phe Tyr Asp Thr Leu Thr Arg Tyr Val Phe Gln Tyr Phe
100 105 110

Asp His Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr
130 135 140

Thr Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Glu Arg
145 150 155 160

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val
165 170 175

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr
180 185 190

Gly Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

Lys Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
210 215 220

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr
225 230 235 240

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
245 250

<210> 17

<211> 251

<212> PRT

<213> Homo sapiens

<400> 17

Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys

ETABLISSEMENTS ABCDEFG
SOCIÉTÉ ANONYME AU CAPITAL DE 300 000 F
20, RUE DU XVUTRSTBSL F 00000 NTBCLAG
Tél. : (35) 24 46 32 Adr Tg : NRVLIJROLM
Télex : 31596 F IN 718490070257
Transporteur (ou Transitaire)
M. M. DUPONT Frères
8 quai des bldfsh F 0000 NTBCLAG

Mot directeur

CLASSEMENT	FACTURE INVOICE	Exemplaire 15	
CODE CLIENT Z 04399	DATE 7-7-74	NUMÉRO 06	FEUILLET 01
Votre commande	du 74-2-2uméro 438		
Notre offre AZ/B7	du 74-1-1uméro 12		

LIVRAISON

5, rue XYZ
99000 VILLE

FACTURATION

12, rue ABCD BP 15
99000 VILLE

DOMICILIATION BANCAIRE DU VENDEUR

CODE BANQUE CODE GUICHET COMPTE CLIENT

ORIGINE

Pays 1

TRANSPORTS
DESTINATION

Etat 2

MODE

Air

PAYS D'ORIGINE

PAYS DE DESTINATION

CONDITIONS DE LIVRAISON

DATE 74-03-03

LICENCE D'EXPORTATION

NATURE DU CONTRAT (monnaie)

CONDITIONS DE PAIEMENT

FAB
(échéance, %)

MARQUES ET NUMÉROS MARKS AND NUMBERS		NOMBRE ET NATURE DES COLIS DÉNOMINATION DE LA MARCHANDISE NUMBER AND KING OF PACKAGES: DESCRIPTION OF GOODS		NOMEN- CLATURE STATISTICAL No	MASSE NETTE NET WEIGHT MASSE BRUTE GROSS WEIGHT	VALEUR VALUE DIMENSIONS MEASURE- MENTS
74.21.456.44.2 A		1 Composants		U 123/4	5 kg 8 kg	1400 X 13x10x6
QUANTITÉ COMMANDEE ET UNITÉ QUANTITY ORDERED AND UNIT	N° ET RÉF DE L'ARTICLE	DÉSIGNATION		QUANTITÉ LIVRÉE ET UNITÉ QUANTITY DELIVERED AND UNIT	PRIX UNITAIRE UNIT PRICE	MONTANT TOTAL TOTAL AMOUNT
2	AF-809	Circuit intégré		2	104,33 F	208,66 F
10	S8-T4	Connecteur		10	83,10 F	831,00 F
25	ZI07	Composant indéterminé		20	15,00 F	300,00 F

Costs	Débours	Inclus	Non Inclus
Packing	Emballages		92,14
Freight	Transport		
Insurance	Assurances		
Total Invoice amount	Montant total de la facture	1431,80	
Installment	Acomptes		
NET TO BE PAID	NET A RÉGLER	1431,80	

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Pro Phe Tyr Asp Thr Leu Thr Arg Tyr Val Phe Gln Val Trp
 100 105 110

Val Ala Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr
 130 135 140

Thr Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Glu Arg
 145 150 155 160

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val
 165 170 175

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr
 180 185 190

Gly Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser
 195 200 205

Lys Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
 210 215 220

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr
 225 230 235 240

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
 245 250

<210> 19

<211> 251

<212> PRT

<213> Homo sapiens

<400> 19

Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Pro Phe Tyr Asp Thr Leu Thr Arg Tyr Val Phe Gln Val Trp
100 105 110

Val Ala Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr
130 135 140

Thr Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Glu Arg
145 150 155 160

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val
165 170 175

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr
180 185 190

Gly Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
210 215 220

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr
225 230 235 240

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
 245 250

<210> 20
 <211> 251
 <212> PRT
 <213> Homo sapiens

<400> 20
 Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His
 20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
 35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Pro Phe Tyr Asp Thr Leu Thr Gly Tyr Val Phe Gln Val Trp
 100 105 110

Val Ala Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr
 130 135 140

Thr Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Glu Arg
 145 150 155 160

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val
 165 170 175

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr
 180 185 190

Gly Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser
 195 200 205

Lys Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
 210 215 220

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr
 225 230 235 240

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
 245 250

<210> 21
 <211> 251
 <212> PRT
 <213> Homo sapiens

<400> 21
 Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His
 20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
 35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Pro Phe Tyr Asp Thr Leu Thr Gly Tyr Val Phe Gln Val Trp
 100 105 110

Val Ala Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr
 130 135 140

646330

Thr Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Glu Arg
145 150 155 160

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val
165 170 175

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr
180 185 190

Gly Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
210 215 220

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr
225 230 235 240

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
245 250

<210> 22
<211> 251
<212> PRT
<213> Homo sapiens

<400> 22
Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Pro Phe Tyr Asp Thr Leu Thr Ser Tyr Val Phe Gln Tyr Phe

Asp His Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr
130 135 140

Thr Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Glu Arg
145 150 155 160

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val
165 170 175

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr
180 185 190

Gly Ala Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
210 215 220

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr
225 230 235 240

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
245 250

<210> 23
<211> 251
<212> PRT
<213> Homo sapiens

<400> 23
Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Pro Phe Tyr Asp Thr Leu Thr Ser Tyr Val Phe Gln Tyr Phe
100 105 110

Asp His Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr
130 135 140

Thr Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Lys Arg
145 150 155 160

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val
165 170 175

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr
180 185 190

Gly Ala Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
210 215 220

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr
225 230 235 240

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
245 250

<210> 24

<211> 251

<212> PRT

<213> Homo sapiens

<400> 24

Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
 210 215 220

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr
 225 230 235 240

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
 245 250

<210> 26
 <211> 251
 <212> PRT
 <213> Homo sapiens

<400> 26
 Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His
 20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
 35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Pro Phe Tyr Asp Thr Leu Thr Arg Tyr Val Phe Gln Tyr Phe
 100 105 110

Asp His Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr
 130 135 140

Thr Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Glu Arg
 145 150 155 160

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val
165 170 175

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr
180 185 190

Gly Ala Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
210 215 220

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr
225 230 235 240

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
245 250

<210> 27

<211> 251

<212> PRT

<213> Homo sapiens

<400> 27

Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Pro Phe Tyr Asp Thr Leu Thr Arg Tyr Val Phe Gln Tyr Phe
100 105 110

Asp His Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly

centrifugation at 3,500 rpm for 10 minutes. The phage-containing supernatants (5 ml) were carefully transferred to a fresh tube.

[0692] For each of the 48 scFvs listed in Table 3, two aliquots of 20 μ l 6xMPBS were pipetted into separate wells of a 96-well plate (Greiner). The first aliquot was supplemented with BLyS to a final concentration of 0.5 μ g/ml. The second aliquot was supplemented with TNF- α to a final concentration of 0.5 μ g/ml. Each experiment was performed in triplicate. One hundred μ l of each phage supernatant was then added to each aliquot and mixed by pipetting up and down. The phage were incubated (\pm competing antigen) at room temperature for 1 hour.

[0693] Flexible 96-well plates (Falcon) were coated overnight at 4°C with 50 μ l of 10 μ g/ml U937 plasma membranes. After coating, the plates were washed 3 times with PBS and blocked for 1 hour at room temperature with 200 μ l MPBS. The plates were washed 3 times with PBS and 50 μ l of phage (\pm competing antigen) was added to each appropriate well. The plates were incubated at room temperature for 1 hour and then washed with 3 changes of PBST followed by 3 changes of PBS. To each well, 50 μ l of a mouse anti-gene VIII-HRP conjugate (Pharmacia) at a 1:5000 dilution in MPBS was added and the plates incubated at room temperature for 1 hour. Each plate was washed three times with PBST followed by three times with PBS. Then 50 μ l of an HRP-labelled anti-mouse polymer (DAKO EnVision) diluted 1:50 in 3% MPBS was added and incubated for 1 hour at room temperature. Each plate was then washed three times with PBST followed by three times with PBS. Fifty μ l of TMB substrate was then added to each well, and incubated at room temperature for 30 to 60 minutes or until color development. The reaction was stopped by the addition of 25 μ l of 0.5 M H₂SO₄. The signal generated was measured by reading the absorbance at 450nm (A₄₅₀) using a microtiter plate reader (Bio-Rad 3550).

[0694] All 48 scFvs bind to U937 plasma membrane preparations. This signal could be competed out by pre-incubation of the phage antibody with BLyS but not by pre-incubation with TNF- α . This indicates that the 48 scFvs specifically recognize membrane-bound BLyS as well as soluble BLyS. Typical results are exemplified by scFvs I031F09, I050A12 and I051C04 and are shown in Figure 4. All 3 scFvs demonstrate binding to U937 plasma membranes. This binding was specifically competed

out with BLyS but did not compete with TNF- α , demonstrating specific recognition of membrane-bound BLyS.

Example 6: scFv Off-rate Determinations

[0695] All off-rate determinations were performed on BIAcore 2000 machines, using the BIAcore 2000 Control Software and evaluated using the BIAevaluation 3.0 software.

Preparation of a Low Density BLyS Surface

[0696] A 500RU surface was prepared for kinetic studies with purified scFvs. A low density BLyS surface (500 RU BLyS coupled) was prepared in flow cell 2 by amine coupling to a CM5 chip. A new CM5 chip was inserted into the BIAcore and a sensorgram initiated with HBS buffer at a flow rate of 5 μ l/min. The NHS and EDC coupling solutions (BIAcore) were mixed according to manufacturer's instructions and 30 μ l injected over the CM5 surface. Fifty μ l of BLyS at 1 μ g/ml in 10 mM sodium acetate buffer, pH4, was then injected followed by 30 μ l of ethanolamine-HCl solution (BIAcore). The flow rate was then adjusted to 20 μ l/min and 10 μ l of 4M guanidine hydrochloride in HBS injected over the surface. This strips the surface of non-covalently bound BLyS.

Measurement of scFv off-rate kinetics on the low density surfaces

[0697] The chip containing the low density BLyS surface was inserted in to the BIAcore. A dilution series of purified scFvs was prepared in HBS, typically 50 μ g/ml doubling dilutions down to 1.5 μ g/ml. The dilution series was then injected sequentially over the low density BLyS surface (and blank control) using the following program:

MAIN

FLOWCELL 1,2,3,4

APROG	genab	r1d1	ab1
APROG	genab	r1d2	ab2
APROG	genab	r1d3	ab3
APROG	genab	r1d4	ab4

APROG	genab	r1d5	ab5
APROG	genab	r1d6	ab6

APPEND CONTINUE

END

DEFINE APROG genab

PARAM %Abpos %AbId

FLOW 20

KINJECT %Abpos 200 80

INJECT r1c6 10!guanidine hydrochloride regeneration step

EXTRACLEAN

END

[0698] Bound scFvs were removed by injecting 10µl 4M GuHCl in HBS over the surface between scFv samples.

[0699] The binding curves for individual scFvs were analyzed using the BIAevaluation software to determine antibody off-rates. Kinetic analysis for a typical scFv antibody, I003C02, is shown in Figure 5. I003C02 has a $K_{\text{off}} = 6 \times 10^{-3} \text{ s}^{-1}$.

Example 7: Inhibition in an *In Vitro* Receptor Binding Assay by scFv Antibodies

[0700] The 48 scFvs listed in Table 3 were purified and assessed for their ability to inhibit BLYS binding to its receptor on IM9 cells.

Purification of scFv

[0701] To determine the inhibitory potency of anti-BLYS scFv, scFv's were first prepared by IMAC. 2TYAG (5 ml) was inoculated with a single colony and grown overnight at 30°C, shaking. This overnight culture was then used to inoculate 500 ml of 2TY containing 100 µg/ml ampicillin and 0.1% Glucose, and grown at 30° C, shaking, until an A_{600} of 1.0 was attained. IPTG was added to 1 mM and the culture was grown for a further 3.5 hours at 30°C.

[0702] Cells were harvested by centrifugation at 5,000rpm, and resuspended in 10 ml of TES. A further 15 ml of a 1:5 dilution (in water) of TES was added, and the cell suspension incubated on a turning wheel at 4°C for 30 minutes. This causes osmotic shock and yields a periplasmic extract containing the scFv. Residual cells and debris were pelleted by centrifugation at 9,000 rpm for 20 minutes at 4°C. The supernatant was transferred to a new tube, and 50 µl of 1 M MgCl₂ added. Two ml of a Ni-NTA agarose (Qiagen), pre-washed with buffer (50 mM sodium phosphate, pH 8, 300 mM NaCl) together with a protease inhibitor tablet (Boehringer Mannheim) were then added to the periplasmic extract. The preparation was incubated, rotating, overnight at 4°C. The Ni-NTA was pelleted by centrifugation at 2,000 rpm for 5 minutes, and the supernatant was aspirated. The agarose beads were washed 3 times with 50 ml wash buffer, centrifuging to collect the agarose in between each wash. Ten ml of wash buffer was added after the final wash, and the slurry was loaded on to a polyprep column (BioRad). Two ml elution buffer (50 mM NaPi (sodium phosphate), pH 8, 300 mM NaCl, 250 mM imidazole) was added to the drained agarose, and the eluate was collected. IMAC purified scFv was buffer exchanged in to PBS by use of a Nap 5 column (Pharmacia) according to the manufacturer's instructions. The A₂₈₀ was read and the protein concentration determined using a molar extinction coefficient of 1 mg/ml protein = A₂₈₀ 1.4. Purified scFv was stored in 500 µl aliquots at -70°C.

Receptor Binding Inhibition Assay

[0703] Flat-bottomed 96-well plates (Costar) were coated with 100 µl per well of a 1:10 dilution of poly-L-lysine (Sigma) in PBS for 1 hour at room temperature. The plates were then washed twice with water, allowed to air-dry and placed at 4 °C overnight. One hundred µl of IM9 cells (at 10⁶/ml in RPMI-1640) were then added to each well. Plates were then centrifuged at 3200 rpm for 5 mins to pellet the cells. The media was carefully aspirated and 200 µl of MPBS added to each well. The plates were then left to block for 1 hour at room temperature.

[0704] To a separate 96-well plate, titrate test scFvs in MPBS, in triplicate, over a concentration range from 10 µg/ml down to 0.001 µg/ml were added. The final volume of test scFv in each well was 55 µl. Competition with unlabelled BLYS was also included in every assay as a control. Unlabelled BLYS, in MPBS, was typically titrated in triplicate,

over a concentration range from 1 µg/ml down to 0.001 µg/ml. 10 µl of biotinylated-BLyS (at 162.5 ng/ml) in MPBS was added to each well to give a final concentration of 25 ng/ml. Plates were then incubated at room temperature for 30 minutes.

[0705] The IM9 coated plates was washed twice in PBS, tapped dry and immediately 50µl of the scFv/biotinylated-BLyS mix was added and incubated at room temperature for 1 hour. Plates were washed three times in PBST and three times in PBS, tapped dry and 50 µl per well added of streptavidin-Delfia (Wallac) at 1:1000 dilution in the Manufacturer's assay buffer. The plates were then incubated at room temperature for 1 hour and washed six times in Delfia wash solution (Wallac). After tapping the plates dry, 100µl per well of Delfia enhancement solution (Wallac) was added. The plates were gently tapped to encourage micelle formation, incubated at room temperature for 10 minutes, and fluorescence read on a Wallac 1420 workstation at 6520 nM.

[0706] Typical titration curves for two scFv antibodies, I007F11 and I050A07, are shown in Figure 6. Unlabelled BLyS competed for binding to its receptor with an IC₅₀ value of 0.8 nM. The IC₅₀ values for I007F11 and I050A07 are 7.9 nM and 17.1 nM , respectively. The assay was performed in triplicate and standard error bars are shown. The 9 scFvs that demonstrated the greatest inhibition as scFv are listed in Table 4. This data also confirms that these 9 scFvs recognize the soluble form of BLyS.

Table 4: 9 ScFvs that demonstrated greatest potency in BLyS Receptor Binding Inhibition Assay

ScFv Antibody
I017D10
I022D01
I008A11
I006D08
I031F02
I050A12
I050B11
I051C04

Example 8: Antibodies recognizing a soluble form of BLyS

[0707] A library of phage was screened in an assay to identify those phage displaying scFvs that immunospecifically bind to the soluble but not the membrane-bound forms of BLyS.

[0708] A phage library was screened for the ability to bind to biotinylated BLyS. The phage were exposed to biotinylated BLyS, allowed an interval of time to bind the biotinylated BLyS. Phage binding bio-BLyS were then isolated by capture on streptavidin coated magnetic beads.

[0709] The phage identified in the screen above (capture of Bio-BLyS from solution) were then screened by ELISA for their ability to bind immobilized BLyS. The scFv expressed by phage that bound immobilized BLyS were then cloned and sequenced. Again, several sequences were identified multiple times, thus a panel (panel 2) consisting of an example of each phage expressing a unique scFv was then characterized further.

[0710] The derived amino acid sequences of these scFvs are shown in Table 1 above. The individual V_H and V_L segments of the scFvs were aligned to the known human germline sequences in V-BASE (Tomlinson et al, www.mrc-cpe.cam.ac.uk) and the closest germline identified.

Example 9: Specificity For Soluble BLyS

[0711] The scFvs were isolated from a library of phage based on their ability to bind a soluble form of BLyS. Briefly, phage were preincubated with biotinylated BLyS in solution. Phage that bound to this biotinylated BLyS were then isolated using streptavidin coated magnetic beads.

[0712] The specificity of each of the unique scFvs for BLyS and for the membrane-bound form of BLyS, was determined by phage ELISA. BLyS was immobilised onto plastic as a purified soluble form of the protein or as a membrane-bound form present on plasma membrane preparations from the human macrophage-like cell line, U937. Maintenance of U937 cells and plasma membrane preparations were performed as detailed in Example 2.

Phage ELISA

[0713] To determine the specificity of each of the scFvs, a phage ELISA was performed for each antibody against human BLyS, U937 plasma membranes, TNF α , BSA and an uncoated well. Antigen coating conditions were as described in Example 2, apart from human BLyS. BLyS was first biotinylated (as described in Example 3) and coated at 1 μ g/ml onto streptavidin coated plates (Reacti-Bind, Pierce) for 30 mins at room temperature. The plates were then washed, blocked and the phage ELISA performed as detailed in Example 2.

[0714] The results for 3 clones (I074B12, I075F12 and I075A02) that bind the soluble but not the membrane-bound form of BLyS are shown in Figure 7. As a control, a phage antibody that recognizes TNF α , is also shown in Figure 7. There is a small non-specific background signal on the U937 plasma membranes that is evident with both the anti-BLyS scFvs as well as the anti-TNF α control. All 3 anti-BLyS scFvs recognize BLyS but not U937 plasma membranes, TNF α , BSA or an uncoated well (PBS only). This indicates that the scFvs do not bind the membrane-bound form of BLyS. Further, The fact that these scFvs were isolated on the basis of their ability to bind soluble biotinylated BLyS indicates that they bind the soluble form of BLyS. Further confirmation of these scFvs' specificity for BLyS is provided in Example 10.

Example 10: Inhibition in an *in vitro* receptor binding assay by phage scFvs

[0715] All of the unique phage scFvs from panel 2 were assessed for their ability to inhibit BLyS binding to its cognate receptor on IM9 cells. The biotinylation of BLyS, maintenance of IM9 cells and receptor binding inhibition assay were performed as described in Example 3.

[0716] Results for two phage scFvs, I0025B09 and I026C04 are shown in Figure 8. Maximal binding of biotinylated BLyS to its receptor (bio-BLyS only), the background signal in the absence of biotinylated BLyS (no bio-BLyS), and results with an irrelevant (i.e. does not recognize BLyS) phage antibody are also shown. Both phage scFvs inhibited biotinylated BLyS binding to its receptor on IM9 cells. 33 of the unique scFvs from panel 2 were identified for further study. These 33 scFvs demonstrated the greatest inhibition as phage particles in this assay and are listed in Table 5.

Table 5: Identification of 33 phage scFvs to free BLyS that demonstrate the most significant inhibition of biotinylated-BLyS binding to its receptor

Antibody	Antibody	Antibody	Antibody
I026C04	I074B12	I073F04	I065D04
I003C06	I075A02	I078D08	I068C08
I025B09	I068B08	I078D02	I068F03
I027B12	I068B04	I075G01	I069B07
I025B06	I068C06	I071B03	
I030A10	I075F12	I072B09	
I002A01R	I065D08	I078H08	
I002A01K	I065F08	I064C04	
I026C04R	I067B10	I064C07	
I026C04K	I067F05		

Example 11: Specificity of anti-BLyS scFvs

[0717] The specificity of the 33 scFvs (listed in Table 5) for immobilized human and murine BLyS was determined using phage ELISA.

Phage ELISA

[0718] To determine the specificity of the 33 scFvs, a phage ELISA was performed as described in Example 4 against human and mouse BLyS, and a panel of related human antigens: TRAIL, LIGHT, TNF α , TNF β , and an uncoated well (PBS only).

[0719] Typical results for two scFvs, I067F05 and I078D02 are shown in Figure 9. A control antibody that specifically recognizes TNF α is also shown. Both anti-BLyS scFvs specifically recognize immobilized human and mouse BLyS but not any other antigen tested.

[0720] All 33 scFvs are specific for human BLyS. 14/33 cross-react with mouse BLyS but not with any other unrelated or related antigen tested.

Example 12: scFv Off-Rate Determinations

[0721] Off-rate determinations, preparation of a low density BLyS surface and kinetic measurements were as detailed in Example 6.

[0722] The binding curves for individual scFvs were analysed using the BIAevaluation software to determine antibody off-rates. Kinetic analysis for a typical scFv antibody, I002A01, is shown in Figure 10. I002A01 has a $K_{\text{off}} = 9 \times 10^{-4} \text{ s}^{-1}$.

Example 13: Inhibition in an *in vitro* receptor binding assay by scFv antibodies

[0723] The 33 scFvs identified in Table 5 were prepared as purified scFvs and assessed for their ability to inhibit BLYS binding to its receptor on IM9 cells. The scFvs were purified and analysed in the receptor binding inhibition assay as described in Example 6.1.8.

[0724] Typical titration curves for two scFvs, I0068C06 and I074B12, are shown in Figure 11. Unlabelled BLYS competed for binding to its receptor with an inhibitory constant 50 (IC_{50}) value of 0.66 nM. The IC_{50} values for I0068C06 and I074B12 are 61 nM and 13 nM, respectively. The assay was performed in triplicate and standard error bars are shown. The 7 scFvs that demonstrated the greatest inhibition as scFv are listed in Table 6.

Table 6: Identification of 7 scFvs to free BLYS that demonstrate the most significant inhibition of biotinylated-BLYS binding to its receptor as purified scFv's.

Antibody
I002A01-R
I002A01-K
I026C04-R
I026C04-K
I068C06
I075F12
I067B10

Example 14: ScFvs Recognizing Membrane-bound BLYS

[0725] A library of phage was screened in an assay to identify those phage displaying scFvs that immunospecifically bind to the membrane-bound but not the soluble form of BLYS.

[0726] As a starting point, a library of phage expressing scFv antibodies were panned on immobilized HIS-tagged BLYS. Phage isolated by panning were then screened for the ability to bind to HIS-tagged BLYS. HIS-tagged BLYS was obtained by expressing amino acids 71-285 of SEQ ID NO:3228 using the pQE9 vector (Qiagen Inc.,

Valencia, CA) in *E. coli* and purifying the expressed protein. This phage clones identified by this screen were then sequenced. After sequencing, A panel (panel 3) of phage each expressing a unique scFv that bound HIS-tagged BLyS was generated and further characterized.

[0727] The derived amino acid sequences of the unique scFvs from panel 3 are shown in Table 1 above. The individual V_H and V_L segments of the scFvs were aligned to the known human germline sequences in V-BASE (Tomlinson et al, www.mrc-cpe.cam.ac.uk) and the closest germline identified.

Example 15: Recognition of Membrane-bound BLyS

[0728] The specificity of each of the unique scFvs for both the membrane-bound form of BLyS as well as for the soluble form of BLyS, was determined by phage ELISA.

[0729] BLyS was immobilised onto plastic either directly as a purified soluble form of the protein or biotinylated and coated on a streptavidin plate as in Example 9. Binding to HIS-tagged BLyS was used as a primary screen for scFv's that would bind the membrane-bound form of BLyS (see below). The membrane-bound form of BLyS was presented as plasma membranes preparations from the human macrophage-like cell line, U937 or the murine cell line P388.

[0730] Mouse monoclonal antibodies have been raised against His-tagged BLyS according to standard procedures. Characterization of these mouse monoclonal antibodies revealed that they specifically recognized both His-tagged BLyS and the membrane-bound form of BLyS on U937 cells, but not soluble BLyS. Therefore, specific recognition of His-tagged BLyS was used as supporting evidence for the recognition of the membrane-bound form of BLyS by phage and scFv antibodies.

Phage ELISA

[0731] To determine the specificity of each of the scFvs, a phage ELISA was performed for each antibody against His-tagged human BLyS, U937 plasma membranes, TNF α , BSA and an uncoated well. Antigen coating conditions were as described in 2. apart from human BLyS. BLyS was first biotinylated (as described in Example 3) and coated at 1 μ g/ml onto streptavidin coated plates (Reacti-Bind, Pierce) for 30 mins at room temperature. The plates were then washed, blocked and the phage ELISA performed as

detailed in Example 2.

[0732] The results for 3 clones, I079C01, I081C10 and I082A02, and a control phage antibody that recognizes TNF α , are shown in Figure 12. All 3 scFvs recognize U937 plasma membranes (U937) and His-tagged BLyS (HIS-BLyS) but not, biotinylated BLyS (bio-BLyS) or an uncoated well (PBS). This indicates that the scFvs recognize the membrane-bound form of BLyS.

Example 16: Specificity for Membrane-bound BLyS

[0733] The specificity of the scFvs for only the membrane-bound form of BLyS, and not for the soluble form, was confirmed using a competition ELISA. This assay assesses the ability of test phage scFvs to bind to the membrane-bound form of BLyS on U937 plasma membranes in the presence of different forms of competing BLyS.

Competing BLyS was either the His-tagged form of BLyS or soluble BLyS. ScFvs specific for the membrane-bound BLyS would be expected to be competed out by pre-incubation with His-tagged BLyS but not by pre-incubation with soluble BLyS.

[0734] Maintenance of U937 cells and plasma membrane preparations were performed as detailed in Example 2.

Competition ELISA

[0735] U937 plasma membranes (50 μ l per well) were coated at 10 μ g/ml in PBS onto Falcon 96-well plates overnight at 4°C.

[0736] Individual *E. coli* colonies containing a phagemid representing one of the unique scFvs from the panel 3 were inoculated into 50 ml tubes (Falcon) containing 5 ml 2TYAG medium. Tubes were incubated at 37°C for 4 hours, shaking. M13KO7 helper phage was added to each tube to an MOI of 10 and the tubes were incubated for a further 1 hour at 37°C. The tubes were centrifuged in a benchtop centrifuge at 3500 rpm for 10 minutes. The supernatant was removed and cell pellets were resuspended in 5 ml 2TYAK and incubated at 30°C overnight, shaking. The next day, tubes were centrifuged at 3500 rpm for 10 min and the phage-containing supernatant carefully transferred into a fresh tube.

[0737] For each test phage antibody, 3 aliquots of 20 μ l 18% marvel/6xPBS were transferred into separate wells of a 96-well plate. The first aliquot was supplemented with

His-tagged BLyS to a final concentration of 60 µg/ml. The second aliquot was supplemented with soluble BLyS to a final concentration of 60 µg/ml. The third aliquot was not supplemented with any competing antigen. One hundred µl of phage supernatant was then added to each aliquot and left to block at room temperature for 1 hour.

[0738] The antigen-coated plates were washed once with PBS before the addition of 200 µl/well 3% marvel/PBS. These plates were left to block at 37°C for 1 hour and were then washed once with PBS. Duplicate samples of 50 µl pre-blocked phage (above) were added to the antigen-coated plates and left at room temperature for 1 hour. Plates were washed 3x with PBS/0.1%Tween 20, then 3x with PBS. Fifty µl/well mouse anti-M13 HRP (Pharmacia) at 1/5000 in 3% Marvel/PBS was added and left for 1 hour at room temperature. Plates were washed 3 times with PBS/0.1%Tween 20, then 3 times with PBS. Fifty µl/well HRP-labelled anti-mouse Envision polymer (DAKO) at 1/50 in 3% marvel/PBS was added and left for 1 hour at RT. Plates were washed 3 times with PBS/0.1% Tween 20, then 3 times with PBS. Next, 50µl/well of TMB (Sigma) was added and plates left to develop for 30 to 60 minutes. When sufficient color has developed, 25µl/well 0.5M H₂SO₄ was added to stop the reaction. The plates were read at 450nm on a microtiter plate reader (Bio-Rad 3550).

[0739] The results for 3 clones, I079B04, I079F08 and I080B01, and a control phage antibody that recognizes TNFα, are shown in Figure 13. All 3 scFvs recognize U937 plasma membranes (U937). This binding is competed out to background levels (i.e. comparable to the signal observed with the anti-TNFα phage antibody) in the presence of His-tagged BLyS (HIS-BLyS) but not biotinylated BLyS (bio-BLyS). This confirms that the scFvs specifically recognize the membrane-bound form but not the soluble form of BLyS.

Example 17: High Throughput BIAcore Screen to identify high affinity scFvs

[0740] This is a 96-well screen where the test samples (scFvs) are derived from 1 ml periplasmic extracts of individual antibody expressing clones. Potentially higher affinity scFvs are then identified principally as those giving a large number of total RU's bound to a HIS-BLyS surface in BIAcore. This method of ranking does assume approximately equal yields of scFv from each clone. Since this is not always the case,

some scFvs may also be identified that simply express high levels of scFv. These can be discriminated from those of higher affinity by further characterization of the scFvs (see Example 18).

Preparation of ScFv from 1ml E.coli Cultures

[0741] Individual E.coli colonies containing a phagemid representing one of the unique scFvs from panel 3 were inoculated into 96-well plates containing 100 μ l 2TYAG medium per well. Eight wells on each plate were reserved for positive and negative control samples. The plate was grown overnight at 30°C with shaking at 120 rpm.

[0742] Next day, 1ml of 2TYAG + 345 mM sucrose was added to each well of an autoclaved 96 deep well plate (Beckman). Twenty μ l of each overnight culture was resuspended and transferred to the appropriate well of the deep well plate. The plate was grown for approximately 3.5 hours at 30°C with shaking at 250 rpm (or until the OD₆₀₀ = 0.6). Fifty μ l of 1M IPTG was added to 5ml 2TY and 10 μ l of this was added to each well. The plate was grown overnight at 30°C with shaking at 250rpm.

[0743] Plates were kept at 4°C for the remainder of the procedure. The overnight plate (above) was centrifuged at 3500 rpm for 10 minutes at 4°C to pellet the cells. The supernatant was decanted and each pellet resuspended in 100 μ l TES (0.2M Tris HCl pH8.0, 0.5mM EDTA, 0.5M sucrose) and transferred to a fresh 96 well plate. This plate was incubated on ice for 30 minutes and then centrifuged for 10 minutes at 3500 rpm at 4°C to pellet the cell debris. During centrifugation, 15 μ l of freshly made protease inhibitors cocktail (Roche, 1 tablet dissolved in 1.5 ml water) was added to each well of a fresh 96 well plate. Supernatants from the centrifuged plate were then transferred to the plate containing the protease inhibitors. The plate was centrifuged at 3500 rpm for 10 minutes at 4°C and the supernatant was transferred to a further 96-well plate. This step was repeated at least once more or until there was no sign of any cell debris following centrifugation. Finally, the plate was covered in foil to prevent evaporation of samples during the BIAcore run.

Generation of a high density HIS-BLyS surface

[0744] All BIAcore analysis was performed on BIAcore 2000 machines, using the BIAcore 2000 control software and evaluated using the BIAevaluation 3.0 software. A

high density His-tagged BLyS surface (>1000 RU HIS-BLyS coupled) was prepared in flow cell 2 by amine coupling to a CM5 chip. A new CM5 chip was inserted into the BIAcore and a sensorgram started over flow cell 2 with HBS buffer at a flow rate of 5µl/min. The NHS and EDC solution were mixed 1:1 before injecting 30µl over the CM5 surface. Fifty µl HIS-BLyS (at 10µg/ml in Sodium acetate buffer, pH4) was injected and allowed to couple to the surface. Thirty µl of ethanolamine-HCl solution was then injected to block free NHS esters. Prior to using the chip, 10µl of 4M Guanidine hydrochloride in HBS was injected over the surface to strip the surface of non-covalently bound BLyS. A blank surface (no HIS-BLyS) was also prepared over flow cell 1 so that non-specific binding effects can be subtracted from the HIS-BLyS binding curves.

[0745] Typically, a 5000 RU His-tagged BLyS surface was generated in this way and used for 96-well analysis of scFvs isolated from the periplasm of E.coli.

BIAcore Analysis

[0746] The 96-well plate containing periplasmic scFvs was secured inside the BIAcore. Two ml of 4M Guanidine hydrochloride in HBS was placed in a rack inside the BIAcore for regeneration of the HIS-BLyS surface between samples. The sensorgram was run over flow cells 1 and 2 at a flow rate of 20µl/minute. The following method was run:

MAIN

FLOWCELL 1,2,3,4

LOOP cycle STEP

APROG inj %pos

ENDLOOP

APPEND CONTINUE

END

DEFINE LOOP cycle

LPARAM %pos


```

rla1
rlb1
rlc1
rld1
rle1
r1f1 etc (all wells listed until r1h12)

```

```

END
DEFINE APROG inj
PARAM %pos
FLOW 20
KINJECT %pos 35 30 !scfv injection
QUICKINJECT r2f3 10 !regeneration
EXTRACLEAN
END

```

[0747] When the run had finished, the sensorgram data for flow cell 1 was subtracted from the data for flow cell 2 for each sample using the BIAevaluation software. The clones were compared with one another principally by overall RU change as the scFv dissociates from the surface. In addition a few scFvs were identified as having potentially slower off-rates. An example of the dissociation section of a typical sensorgram for 8 scFvs is shown in Figure 14. An anti-TNF α antibody that does not recognize BLYS was included as a control. Of the 8 scFvs exemplified, I079F06 was identified for further study due to the relatively high numbers of RU's bound to the surface.

[0748] ScFvs were identified principally if they demonstrated a RU change of over 1200, a few were also identified as having potentially slower than typical off-rates. A total of 28 clones were chosen on these criteria and are listed in Table 7.

Table 7: Identification of 28 antibodies to membrane-bound BLYS that demonstrate the most significant RU changes by BIAcore

Antibody	Antibody
I079C01	I084C04
I082H08	I080E05
I079E02	I083B12
I079B05	I082G01
I079F06	I082G02
I079F08	I082C03
I079F11	I082A05
I079B12	I082D07
I080B01	I082B08
I080G09	I084A01
I099D03	I084B02
I080D03	I080A08
I080A03	I084C11
I083G03	
I080G07	

Example 18: scFv Affinity Determinations

[0749] The affinity (K_D) of the 28 scFvs was determined using the BIAcore.

Low Density HIS-BLyS Surface for Kinetic Studies

[0750] 500RU surfaces were used for kinetic studies of purified scFv binding to HIS-BLyS. The method to prepare these surfaces was identical to the method described in Example 17, only smaller volumes of HIS-BLyS were injected.

Measurement of scFv Binding Kinetics

[0751] The chip containing the low density HIS-BLyS surface was inserted into the BIAcore. A dilution series for each of the 28 purified scFvs (prepared as in Example 6) were diluted in HBS (typically starting with 50 μ g/ml scFv and double diluting down to 1.5 μ g/ml). The dilution series was then injected sequentially over the blank control (flow cell 1) and low density HIS-BLyS surface (flow cell 2) using the following program:

MAIN

FLOWCELL 1,2,3,4

APROG	genab	r1d1	ab1
APROG	genab	r1d2	ab2
APROG	genab	r1d3	ab3

```

APROG      genab      r1d4  ab4
APROG      genab      r1d5  ab5
APROG      genab      r1d6  ab6

```

APPEND CONTINUE

END

```

DEFINE APROG genab
PARAM %Abpos %AbId
FLOW      20
KINJECT   %Abpos 200 80
INJECT    r2f3 10
EXTRACLEAN
END

```

[0752] Bound scFv were removed by injecting 10µl of 4M Guanidine hydrochloride in HBS (location r2f3 in the above program) over the surface between samples. Binding curves for individual scFv were analysed using the BIAevaluation software to determine antibody on- and off-rates.

[0753] A typical example of the binding curves generated for the scFv antibody I082C03 is shown in Figure 15. The off-rate for this clone was calculated as $2 \times 10^{-3} \text{ s}^{-1}$. The affinity of I082C03 was calculated as 20 nM, assuming 100% activity of the scFv. The 5 scFvs with the highest affinities as scFvs are given in Table 8.

Table 8: Identification of 5 antibodies to membrane-bound BLyS that have the highest affinities as scFvs

Antibody	Affinity (K _D)
I079F11	5nM
I079E02	10nM
I082G02	6nM
I082H08	1nM
I099D03	4nM

Example 19: Recognition of mouse membrane-bound BLyS

[0754] The ability of the 5 scFvs listed in Table 8 to also recognize murine membrane-bound BLyS was determined using a competition ELISA. This assay assesses the ability of test phage scFvs to bind to the membrane-bound form of BLyS on the murine cell line, P388, plasma membranes in the presence of different forms of competing human BLyS. Competing BLyS was either presented as the His-tagged form of BLyS, or soluble BLyS. ScFvs that recognize mouse membrane-bound BLyS would give an ELISA signal on the P388 plasma membranes that is competed out by pre-incubation with HIS-tagged BLyS but not by pre-incubation with soluble BLyS.

Maintenance of P388.D1 cells and preparation of plasma membranes

[0755] P388.D1 cells are a mouse monocyte-macrophage like cell line. They were cultured in L-15 medium supplemented with 2mM L-glutamine, 10% CS, 10U penicillin, 100g/ml streptomycin (all reagents from Sigma). Cells were split 1:4 every 3-4 days to maintain a cell density of $2-8 \times 10^5$ per ml. A fresh aliquot of cells was thawed from liquid nitrogen every 6 weeks. Plasma membrane fractions were prepared as described in Example 2.

Competition ELISA

[0756] P388 plasma membranes (50 μ l per well) were coated at 10 μ g/ml in PBS onto Falcon 96-well plates overnight at 4°C. The method is otherwise essentially as described Example 16.

[0757] The results for 3 clones, I079E02, I082H08 and I099D03 are shown in Figure 16. All 3 scFvs recognize P388 plasma membranes. This binding is competed out in the presence of HIS-tagged BLyS (HIS-BLyS) but not in the presence of biotinylated BLyS (bio-BLyS). This confirms that these scFvs also recognize the membrane-bound form but not the soluble form of mouse BLyS.

Example 20 : Conversion of scFvs to IgG1 format

[0758] The VH domain and the VL domains of scFvs that we wished to convert

into IgG molecules were cloned into vectors containing the nucleotide sequences of the appropriate heavy (human IgG1) or light chain (human kappa or human lambda) constant regions such that a complete heavy or light chain molecule could be expressed from these vectors when transfected into an appropriate host cell. Further, when cloned heavy and light chains are both expressed in one cell line (from either one or two vectors), they can assemble into a complete functional antibody molecule that is secreted into the cell culture medium. Methods for converting scFvs into conventional antibody molecules are well known within the art.

Generation of NS0 cell lines expressing anti-BLyS antibodies (IgG1)

[0759] Plasmids containing the heavy and light chains were separately linearized using the Pvu I restriction enzyme. The linearized DNAs were purified by phenol-chloroform extraction followed by ethanol precipitation and then resuspended in H₂O. NS0 cells (10⁷) from a growing culture were electroporated (0.25kV and 975μF) in PBS with 12.5 μg linearized heavy chain plasmid DNA and 37.5 μg linearized light chain DNA. The cells were washed in 20 ml non-selective medium (10% FCS in DMEM supplemented with 6mM glutamine, amino acids and penicillin/streptomycin) and then transferred in 12.5 ml medium into a T75cm² flask and incubated overnight at 37 °C, 5% CO₂/air. The day after transfection the cells were resuspended in selective medium containing 1mg/ml geneticin and dispensed into 5 x 96-well plates at 200 μl/well. After 18 days at 37 °C (5% CO₂/air) the colony supernatants were screened by an ELISA that detects assembled human IgG in order to identify colonies expressing IgG. Approximately twenty positive colonies were expanded and adapted to growth in serum-free, selective medium. Duplicate T25cm² flasks were set up. Cells from one flask were frozen down as a stock and cells in the second flask were grown to saturation. The productivity of the saturated cultures was assessed by ELISA. The highest producing cell lines were then selected for large-scale antibody production.

[0760] The above procedure is exemplified for the I006D08 anti-BLyS antibody constructs. Following electroporation and selection of NS0 cells, supernatants from ninety-three wells each containing a single colony were screened by ELISA to detect assembled IgG1, antibody. Twenty-seven of the supernatants were identified as containing IgG. The colonies from 24 of the positive wells were transferred to 1ml

selective medium in a 24-well plate and allowed to grow for 2 days. The 1ml cultures of cells were then added to 4ml selective medium containing reduced serum (0.5% FCS) in a T25cm² flask. When the cultures reached confluency 1 ml cells were diluted in 4ml selective, serum-free medium in a T25cm² flask. At confluency this subculture regime was repeated again. Finally 1ml cells from the culture containing 0.1% FCS was diluted with 9 ml serum-free, selective medium and divided into 2 x T25cm² to form the saturated and stock cultures. The stock cultures were frozen down and stored in liquid nitrogen once the cultures were confluent. The saturation culture was grown until the viability of the culture was < 10%. Twenty-three out of the 24 colonies originally expanded were successfully adapted to growth in serum-free medium. The productivity of these serum-free adapted cell lines ranged from 0.3 to 17 µg/ml by ELISA quantification of the saturated, 5ml serum-free cultures. The I006D08-32 cell line produced 17 µg/ml.

Large-scale IgG production

[0761] The highest-producing cell lines were revived from frozen stocks and then expanded to 400ml in selective, serum-free medium in 2 liter roller bottles. The cells were grown at 37 °C and rolled at 4 rpm with the headspace being re-equilibrated with 5% CO₂/air every 2-3 days. Finally the culture was expanded to a 4 liter volume by the addition of serum-free medium without selection (400 ml per 2 liter roller bottle). The cultures were then grown to saturation.

[0762] This procedure is exemplified by the production of I006D08 antibody from the I006D08-32 cell line. The frozen stock of I006D08-32 was revived into a T25 cm² containing 5 ml serum-free medium containing 1mg/ml geneticin and grown at 37 °C in 5% CO₂/air incubator. After two days growth the culture was diluted with 7.5 ml fresh medium and transferred to a T75cm² flask. After a further three days in the incubator the cells were transferred to 130 ml selective medium and transferred to a 2 liter roller bottle. After three days growth the cells were diluted with 500 ml selective medium and split into 2 x 2 liter roller bottles. After another 2 days 100 ml fresh selective medium was added to each roller. Finally the next day the culture was expanded to a total volume of 4 liters with non-selective medium and divided into 10 x 2 liter roller bottles. After three days the medium was supplemented with 6mM glutamine. The cells were grown for 17 days from the final subculture into a 4 liter volume. The cells grew up to 3 x10⁶ cells/ml before

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
 35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Pro Phe Tyr Asp Ile Leu Thr Ser Tyr Val Phe Gln Tyr Phe
 100 105 110

Asp His Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr
 130 135 140

Thr Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Lys Arg
 145 150 155 160

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val
 165 170 175

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr
 180 185 190

Gly Ala Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser
 195 200 205

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
 210 215 220

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr
 225 230 235 240

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
 245 250

<210> 30
 <211> 251

<212> PRT
 <213> Homo sapiens

<400> 30

Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His
 20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
 35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Pro Phe Tyr Asp Ile Leu Thr Arg Tyr Val Phe Gln Tyr Phe
 100 105 110

Asp His Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr
 130 135 140

Thr Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Glu Arg
 145 150 155 160

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val
 165 170 175

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr
 180 185 190

Gly Ala Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser
 195 200 205

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
 210 215 220

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr
 225 230 235 240

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
 245 250

<210> 31
 <211> 251
 <212> PRT
 <213> Homo sapiens

<400> 31
 Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His
 20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
 35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Pro Phe Tyr Asp Ile Leu Thr Arg Tyr Val Phe Gln Tyr Phe
 100 105 110

Asp His Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr
 130 135 140

Thr Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Lys Arg
 145 150 155 160

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val
 165 170 175

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr
180 185 190

Gly Ala Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
210 215 220

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr
225 230 235 240

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
245 250

<210> 32

<211> 251

<212> PRT

<213> Homo sapiens

<400> 32

Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Pro Phe Tyr Asp Ile Leu Thr Arg Tyr Val Phe Gln Tyr Phe
100 105 110

Asp His Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr

130 135 140

Thr	Leu	Thr	Gln	Ser	Pro	Asp	Thr	Leu	Ser	Leu	Ser	Pro	Gly	Glu	Arg
145					150					155					160
Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Thr	Arg	Gly	Trp	Val
				165						170				175	
Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	Met	Tyr
			180					185					190		
Gly	Thr	Ser	Arg	Arg	Ala	Thr	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser
		195					200					205			
Glu	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Arg	Leu	Glu	Pro	Glu
	210						215				220				
Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Tyr	Ala	Thr	Ser	Pro	Arg	Thr
225						230				235					240
Phe	Gly	Gln	Gly	Thr	Arg	Leu	Glu	Ile	Lys	Arg					
				245					250						
<210> 33															
<211> 251															
<212> PRT															
<213> Homo sapiens															
<400> 33															
Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Val	Glu	Val	Lys	Lys	Pro	Gly	Ala
1				5					10					15	
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Ser	Asn	His
			20					25					30		
Gly	Ile	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Val
		35					40					45			
Gly	Trp	Ile	Ser	Gly	His	Asp	Asp	Ser	Thr	Lys	Tyr	Ala	Gln	Lys	Phe
	50					55					60				
Gln	Gly	Arg	Val	Thr	Met	Thr	Ala	Asp	Thr	Ser	Thr	Ser	Thr	Ala	Tyr
65					70					75					80
Ile	Glu	Leu	Arg	Ser	Leu	Lys	Ser	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	

Ala Arg Pro Phe Tyr Asp Ile Leu Thr Ser Tyr Val Phe Gln Tyr Phe
100 105 110

Asp His Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr
130 135 140

Thr Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Glu Arg
145 150 155 160

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val
165 170 175

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr
180 185 190

Gly Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
210 215 220

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr
225 230 235 240

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
245 250

<210> 34

<211> 251

<212> PRT

<213> Homo sapiens

<400> 34

Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Pro Phe Tyr Asp Thr Leu Thr Arg Tyr Val Phe Gln Tyr Phe
 100 105 110

Asp His Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr
 130 135 140

Thr Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Lys Arg
 145 150 155 160

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val
 165 170 175

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr
 180 185 190

Gly Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser
 195 200 205

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
 210 215 220

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr
 225 230 235 240

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
 245 250

<210> 35

<211> 251

<212> PRT

<213> Homo sapiens

<400> 35

Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His
 20 25 30
 Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
 35 40 45
 Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
 50 55 60
 Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80
 Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Pro Phe Tyr Asp Ile Leu Thr Ser Tyr Val Phe Gln Tyr Phe
 100 105 110
 Asp His Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly
 115 120 125
 Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr
 130 135 140
 Thr Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Lys Arg
 145 150 155 160
 Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val
 165 170 175
 Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr
 180 185 190
 Gly Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser
 195 200 205
 Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
 210 215 220
 Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr
 225 230 235 240

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
 245 250

<210> 36

<211> 251

<212> PRT

<213> Homo sapiens

<400> 36

Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His
 20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
 35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Pro Phe Tyr Asp Ile Leu Thr Arg Tyr Val Phe Gln Tyr Phe
 100 105 110

Asp His Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr
 130 135 140

Thr Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Lys Arg
 145 150 155 160

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val
 165 170 175

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr
 180 185 190

Gly Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
210 215 220

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr
225 230 235 240

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
245 250

<210> 37

<211> 251

<212> PRT

<213> Homo sapiens

<400> 37

Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Pro Phe Tyr Asp Thr Leu Thr Ser Tyr Val Phe Gln Tyr Phe
100 105 110

Asp His Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr
130 135 140

Thr Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Lys Arg

145		150		155		160
Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val						
	165			170		175
Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr						
	180			185		190
Gly Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser						
	195			200		205
Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu						
	210			215		220
Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr						
	225			230		235
Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg						
	245			250		
<210> 38						
<211> 251						
<212> PRT						
<213> Homo sapiens						
<400> 38						
Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala						
1		5		10		15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His						
	20			25		30
Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val						
	35			40		45
Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe						
	50			55		60
Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr						
	65			70		75
Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys						
	85			90		95
Ala Arg Pro Phe Tyr Asp Thr Leu Thr Ser Tyr Val Leu Gly Tyr Tyr						
	100			105		110

Leu Ser Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr
 130 135 140

Thr Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Glu Arg
 145 150 155 160

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val
 165 170 175

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr
 180 185 190

Gly Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser
 195 200 205

Glu Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
 210 215 220

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr
 225 230 235 240

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
 245 250

<210> 39

<211> 251

<212> PRT

<213> Homo sapiens

<400> 39

Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His
 20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
 35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Pro Phe Tyr Asp Thr Leu Thr Ser Tyr Val Phe Gln Tyr Phe
100 105 110

Asp His Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr
130 135 140

Thr Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Glu Arg
145 150 155 160

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val
165 170 175

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr
180 185 190

Gly Ala Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

Glu Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
210 215 220

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr
225 230 235 240

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
245 250

<210> 40

<211> 251

<212> PRT

<213> Homo sapiens

<400> 40

Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His
 20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
 35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Pro Phe Tyr Asp Thr Leu Thr Ser Tyr Val Phe Gln Val Trp
 100 105 110

Val Ala Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr
 130 135 140

Thr Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Glu Arg
 145 150 155 160

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val
 165 170 175

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr
 180 185 190

Gly Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser
 195 200 205

Glu Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
 210 215 220

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr
 225 230 235 240

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
 245 250

<210> 41
 <211> 251
 <212> PRT
 <213> Homo sapiens

<400> 41
 Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His
 20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
 35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Pro Phe Tyr Asp Ile Leu Thr Ser Tyr Val Phe Gln Tyr Phe
 100 105 110

Asp His Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr
 130 135 140

Thr Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Glu Arg
 145 150 155 160

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val
 165 170 175

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr
 180 185 190

Gly Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser
 195 200 205

Glu Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
 210 215 220

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr
 225 230 235 240

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
 245 250

<210> 42
 <211> 251
 <212> PRT
 <213> Homo sapiens

<400> 42
 Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His
 20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
 35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Pro Phe Tyr Asp Thr Leu Thr Ser Tyr Val Phe Gln Tyr Phe
 100 105 110

Asp His Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr
 130 135 140

Thr Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Glu Arg
 145 150 155 160

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val

165

170

175

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr
180 185 190

Gly Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

Lys Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
210 215 220

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr
225 230 235 240

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
245 250

<210> 43

<211> 251

<212> PRT

<213> Homo sapiens

<400> 43

Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Pro Phe Tyr Asp Thr Leu Thr Ser Tyr Val Phe Gln Tyr Phe
100 105 110

Asp His Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr
 130 135 140

Thr Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Glu Arg
 145 150 155 160

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val
 165 170 175

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr
 180 185 190

Gly Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser
 195 200 205

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
 210 215 220

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr
 225 230 235 240

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
 245 250

<210> 44
 <211> 251
 <212> PRT
 <213> Homo sapiens

<400> 44
 Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His
 20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
 35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80

viability declined to $< 0.2 \times 10^6$ cells/ml. At this low viability the culture supernatants were harvested. ELISA analysis indicated that the culture supernatant contained 33 µg/ml IgG. Hence, the 4 liter culture contained 132 mg IgG.

IgG Purification

[0763] The purification of the IgG from the fermentation broth is performed using a combination of conventional techniques commonly used for antibody production. Typically the culture harvest is clarified to remove cells and cellular debris prior to starting the purification scheme. This would normally be achieved using either centrifugation or filtration of the harvest. Following clarification, the antibody would typically be captured and significantly purified using affinity chromatography on Protein A Sepharose. The antibody is bound to Protein A Sepharose at basic pH and, following washing of the matrix, is eluted by a reduction of the pH. Further purification of the antibody is then achieved by gel filtration. As well as removing components with different molecular weights from the antibody this step can also be used to buffer exchange into the desired final formulation buffer.

Purification of I006D08 IgG1

[0764] The harvest was clarified by sequential filtration through 0.5 µm and 0.22 µm filters. Clarified harvest was then applied to a column of recombinant Protein A Sepharose equilibrated at pH 8.0 and washed with the equilibration buffer. I006D08 antibody was eluted from the Protein A Sepharose by application of a buffer at pH 3.5. The collected antibody containing eluate was then neutralized to pH 7.4 by the addition of pH 8.0 buffer. The neutralized eluate was concentrated by ultrafiltration using a 30 KDa cut off membrane. Concentrated material was then purified by Sephacryl S300HR gel filtration using phosphate buffered saline as the mobile phase. The final monomeric IgG1 fraction from the gel filtration column was then concentrated to the desired formulation concentration by ultrafiltration using a 30 KDa cut off membrane. The final product was filtered through a 0.22 µm filter.

Example 21: Antibody neutralization of murine splenocyte proliferation as measured by ³HdT incorporation

[0765] To determine if an antibody inhibited BLyS mediated B cell proliferation, a splenocyte proliferation assay was performed. Briefly, murine splenocytes were isolated by flushing spleen with complete medium using a 25g needle and 10 ml of complete medium (RPMI 1640 with 10% FBS containing 100U/ml penicillin, 100µg/ml streptomycin, 4mM glutamine, 5x10⁻⁵M β-mercaptoethanol). The cells were passed through a 100 micron nylon filter to remove cell clumps. The cell suspension was then ficolled at 400 x g for 25 minutes at room temperature (one 15 ml conical tube/spleen; 3 ml ficol, 10 ml cell suspension/spleen; Ficoll 1083 from Sigma). The recovered cells were washed 3 times in complete medium and counted. Recovered cells were then diluted to a concentration of 3x10⁶/ml in complete medium containing a 3X concentration of SAC (3X = 1:33,333 dilution of stock) (Staph. aureus Cowan strain; Calbiochem).

[0766] For each antibody, 50 microliters of antibody dilutions at 30µg/ml, 3.0µg/ml, and 0.3µg/ml concentrations were aliquotted into individual wells of a 96 well plate in triplicate. Suitable positive controls, such as, for example monoclonal antibody 15C10, were also used. Medium containing no antibody (and human isotype controls (purchased commercially) when necessary) were used as negative controls.

[0767] BLyS protein was diluted in complete medium to concentrations of 300ng/ml, 90ng/ml and 30ng/ml. 50 microliters of each of the BLyS dilutions were then added to the antibody dilution series in the plates. The plate containing the antibody and BLyS dilutions are then incubated for 30 minutes at 37°C, 5% CO₂, after which 50 microliters of the splenocyte cell suspension containing SAC was added to all wells. The plates were then incubated for 72 hours (37°C, 5% CO₂).

[0768] After 72 hours, each well was supplemented with 50µl of complete medium containing 0.5µCi of ³H-thymidine (6.7 Ci/mM; Amersham) and cells were incubated for an additional 20-24 hours at (37°C, 5% CO₂). Following incubation cells were harvested using a Tomtec Cell Harvester and filters counted in a TopCount Scintillation counter (Packard).

Example 22: Human B cell proliferation assay for in vitro screening of BLyS antagonist

molecules

[0769] The bioassay for assessing the effects of putative BLYS antagonists was performed in triplicate in 96 well format by mixing equal volumes of BLYS, responder cells, and putative antagonist each of which is prepared as a 3X stock reagent.

[0770] B-lymphocytes were purified from human tonsil by MACS (anti-CD3 depletion), washed, and resuspended in complete medium (CM) (RPMI 1640 with 10% FBS containing 100U/ml penicillin, 100µg/ml streptomycin, 4mM glutamine, 5x10E-5 M beta-mercaptoethanol) at a concentration of 3 x 10e6 cells/mL. *Staphylococcus aureus*, Cowan I (SAC, CalBiochem) was added to cells at 3X concentration (3X = 1:33,333 dilution of stock

[0771] Meanwhile, eight serial dilutions (3-fold) of potential antagonist were prepared in CM such that the diluted antagonists are at 3X the final concentrations to be tested in the assay. Antibodies are routinely tested starting at a final concentration of 10ug/mL and going down to about 1.5 ng/mL.

[0772] Human rBLYS was prepared in CM to 3X concentration (3X = 300 ng/mL, 30 ng/mL, and 3 ng/mL) in CM. Potential inhibitors were routinely tested at several concentrations of BLYS to avoid false negatives due to unexpectedly low affinity or antagonist concentration.

[0773] Fifty microliters of diluted antagonist and 50uL of diluted BLYS were added to the putative antagonist dilution series.

[0774] Cells were then incubated for 72 hours (37°C, 5% CO₂) in a fully humidified chamber. After 72 hrs., the cells were supplemented with 0.5 µCi/well 3H-thymidine (6.7 Ci/mmol) and incubated for an additional 24 hours. Plates were harvested using a Tomtec Cell Harvester and filters counted in a TopCount Scintillation counter (Packard).

[0775] The entire disclosure of each document cited (including patents, patent applications, journal articles, abstracts, laboratory manuals, books, or other disclosures) in this application is incorporated in their entireties herein by reference. Further, the sequences disclosed herein are also disclosed in U.S. Provisional Application 60/212,210 filed June 16, 2000 the contents of which are incorporated in their entireties herein by reference.

Table 1: scFvs that Immunospecifically Bind to BLyS

Table 1: scFvs that Immunospecifically Bind to BLyS

Clone ID	scFv SEQ ID NO	AAs of VL	AAs of VL CDR1	AAs of VL CDR2	AAs of VL CDR3	AAs of VH	AAs of VH CDR1	AAs of VH CDR2	AAs of VH CDR3	Sequence (SEQ ID NO)
I003F12S	1	138 - 248	160 - 173	189 - 195	228 - 237	1 - 122	26 - 35	50 - 66	99 - 111	HDDDLVLTGYYPES (SEQ ID NO: 2130)
I006D08	2	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLFPHYGMDV (SEQ ID NO: 2133)
I008A11	3	144 - 254	166 - 179	195 - 201	234 - 243	1 - 128	26 - 37	52 - 69	102 - 117	DRYDILTGYYYGMDV (SEQ ID NO: 2129)
I017D10	4	148 - 255	169 - 179	195 - 201	234 - 244	1 - 132	26 - 35	50 - 66	99 - 121	VQMDSEYYDILLTGINVPYFYFDY (SEQ ID NO: 2132)
I022D01	5	142 - 249	163 - 173	189 - 195	228 - 238	1 - 126	26 - 35	50 - 66	99 - 115	GYYDILTGYYYGMDV (SEQ ID NO: 2135)
I031F02	6	137 - 251	160 - 173	189 - 195	228 - 240	1 - 121	26 - 35	50 - 66	99 - 110	GYYSSAFRAFDI (SEQ ID NO: 2136)
I050A12	7	140 - 250	164 - 174	190 - 196	229 - 239	1 - 124	26 - 35	50 - 66	99 - 113	APYDLLTHFYFYFDY (SEQ ID NO: 2134)
I051C04	8	145 - 256	168 - 181	197 - 203	236 - 245	1 - 129	26 - 35	50 - 66	99 - 118	AATTSQKHNYAYFYGMDV (SEQ ID NO: 2131)
I050B11	9	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTGYVVFQYFDH (SEQ ID NO: 2137)
I050B11-01	10	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTGYVVFQVWVA (SEQ ID NO: 2143)
I050B11-02	11	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTGYVVFQYFDH (SEQ ID NO: 2144)
I050B11-03	12	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTGYVVFQYFDH (SEQ ID NO: 2141)
I050B11-04	13	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTGYVVFQVWVA (SEQ ID NO: 2142)
I050B11-05	14	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTGYVVFQVWVA (SEQ ID NO: 2140)
I050B11-06	15	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTGYVVFQYFDH (SEQ ID NO: 2144)
I050B11-07	16	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTGYVVFQYFDH (SEQ ID NO: 2141)
I050B11-08	17	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTGYVVFQVWVA (SEQ ID NO: 2142)
I050B11-09	18	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTGYVVFQVWVA (SEQ ID NO: 2142)
I050B11-10	19	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTGYVVFQVWVA (SEQ ID NO: 2140)
I050B11-11	20	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTGYVVFQVWVA (SEQ ID NO: 2140)
I050B11-12	21	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTGYVVFQVWVA (SEQ ID NO: 2140)
I050B11-13	22	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTGYVVFQYFDH (SEQ ID NO: 2137)
I050B11-14	23	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTGYVVFQYFDH (SEQ ID NO: 2137)
I050B11-15	24	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTGYVVFQVWVA (SEQ ID NO: 2143)
I050B11-16	25	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTGYVVFQVWVA (SEQ ID NO: 2143)
I050B11-17	26	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTGYVVFQYFDH (SEQ ID NO: 2144)
I050B11-18	27	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTGYVVFQYFDH (SEQ ID NO: 2144)
I050B11-19	28	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTGYVVFQYFDH (SEQ ID NO: 2139)
I050B11-20	29	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTGYVVFQYFDH (SEQ ID NO: 2139)

30	I050B11-21	141-251	166-177	193-199	232-240	1-125	26-35	50-66	99-114	PFYDILTRYVFOYFDH (SEQ ID NO: 2138)
31	I050B11-22	141-251	166-177	193-199	232-240	1-125	26-35	50-66	99-114	PFYDILTRYVFOYFDH (SEQ ID NO: 2138)
32	I050B11-23	141-251	166-177	193-199	232-240	1-125	26-35	50-66	99-114	PFYDILTRYVFOYFDH (SEQ ID NO: 2138)
33	I050B11-24	141-251	166-177	193-199	232-240	1-125	26-35	50-66	99-114	PFYDILTSYVFOYFDH (SEQ ID NO: 2139)
34	I050B11-25	141-251	166-177	193-199	232-240	1-125	26-35	50-66	99-114	PFYDILTRYVFOYFDH (SEQ ID NO: 2144)
35	I050B11-26	141-251	166-177	193-199	232-240	1-125	26-35	50-66	99-114	PFYDILTSYVFOYFDH (SEQ ID NO: 2139)
36	I050B11-27	141-251	166-177	193-199	232-240	1-125	26-35	50-66	99-114	PFYDILTRYVFOYFDH (SEQ ID NO: 2138)
37	I050B11-28	141-251	166-177	193-199	232-240	1-125	26-35	50-66	99-114	PFYDILTSYVFOYFDH (SEQ ID NO: 2137)
38	I093D03	141-251	166-177	193-199	232-240	1-125	26-35	50-66	99-114	PFYDILTSYVVLGYLS (SEQ ID NO: 2145)
39	I093D09	141-251	166-177	193-199	232-240	1-125	26-35	50-66	99-114	PFYDILTSYVFOYFDH (SEQ ID NO: 2137)
40	I093G08	141-251	166-177	193-199	232-240	1-125	26-35	50-66	99-114	PFYDILTSYVFOYVVA (SEQ ID NO: 2143)
41	I097D11	141-251	166-177	193-199	232-240	1-125	26-35	50-66	99-114	PFYDILTSYVFOYFDH (SEQ ID NO: 2139)
42	I1101A04	141-251	166-177	193-199	232-240	1-125	26-35	50-66	99-114	PFYDILTSYVFOYFDH (SEQ ID NO: 2137)
43	I1101B01	141-251	166-177	193-199	232-240	1-125	26-35	50-66	99-114	PFYDILTSYVFOYFDH (SEQ ID NO: 2137)
44	I1101A02	141-251	166-177	193-199	232-240	1-125	26-35	50-66	99-114	PFYDILTSYVFOYFDH (SEQ ID NO: 2137)
45	I1102E01	141-251	166-177	193-199	232-240	1-125	26-35	50-66	99-114	PFYDILTRYVFOYFDH (SEQ ID NO: 2144)
46	I1102G06	141-251	166-177	193-199	232-240	1-125	26-35	50-66	99-114	PFYDILTGVSFQYFDH (SEQ ID NO: 2141)
47	I087A07	141-251	166-177	193-199	232-240	1-125	26-35	50-66	99-114	PFYDILTSYVLPKRVIP (SEQ ID NO: 2227)
48	I087A08	140-250	165-176	192-198	231-239	1-124	26-35	50-66	99-113	PFYDILTSYVCRPHF (SEQ ID NO: 2238)
49	I087A09	140-250	165-176	192-198	231-239	1-124	26-35	50-66	99-113	PFYDILTSYVRCPYV (SEQ ID NO: 2272)
50	I087B02	140-250	165-176	192-198	231-239	1-124	26-35	50-66	99-113	PFYDILTSYVFRPDL (SEQ ID NO: 2281)
51	I087B03	140-250	165-176	192-198	231-239	1-124	26-35	50-66	99-113	PFYDILTSYVKSMPT (SEQ ID NO: 2305)
52	I087B04	140-250	165-176	192-198	231-239	1-124	26-35	50-66	99-113	PFYDILTSYVFPFLYC (SEQ ID NO: 2292)
53	I087B05	140-250	165-176	192-198	231-239	1-124	26-35	50-66	99-113	PFYDILTSYVVPVPST (SEQ ID NO: 2270)
54	I087B06	140-250	165-176	192-198	231-239	1-124	26-35	50-66	99-113	PFYDILTSYVGIHGL (SEQ ID NO: 2282)
55	I087B08	141-251	166-177	193-199	232-240	1-125	26-35	50-66	99-114	PFYDILTSYVPCSPR (SEQ ID NO: 2261)
56	I087B09	140-250	165-176	192-198	231-239	1-124	26-35	50-66	99-113	PFYDILTSYVCYPPA (SEQ ID NO: 2240)
57	I087C02	140-250	165-176	192-198	231-239	1-124	26-35	50-66	99-113	PFYDILTSYVLPLLS (SEQ ID NO: 2224)
58	I087C05	140-250	165-176	192-198	231-239	1-124	26-35	50-66	99-113	PFYDILTSYVALYRL (SEQ ID NO: 2234)
59	I087C06	140-250	165-176	192-198	231-239	1-124	26-35	50-66	99-113	PF

I087D07	66	140 - 250	165 - 176	192 - 198	231 - 239	1 - 124	26 - 35	50 - 66	99 - 113	PFYD TLTSYVPTSTT (SEQ ID NO: 2269)
I087D09	67	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVISCWA (SEQ ID NO: 2299)
I087E04	68	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVSALPPP (SEQ ID NO: 2274)
I087E05	69	140 - 250	165 - 176	192 - 198	231 - 239	1 - 124	26 - 35	50 - 66	99 - 113	PFYD TLTSYVCRHLF (SEQ ID NO: 2236)
I087E10	70	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVVSFSL (SEQ ID NO: 2307)
I087F02	71	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVMGVTPS (SEQ ID NO: 2322)
I087F04	72	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVLFRLPVL (SEQ ID NO: 2326)
I087F05	73	140 - 250	165 - 176	192 - 198	231 - 239	1 - 124	26 - 35	50 - 66	99 - 113	PFYD TLTSYVPSVGG (SEQ ID NO: 2267)
I087F07	74	140 - 250	165 - 176	192 - 198	231 - 239	1 - 124	26 - 35	50 - 66	99 - 113	PFYD TLTSYVPPTRH (SEQ ID NO: 2286)
I087F08	75	140 - 250	165 - 176	192 - 198	231 - 239	1 - 124	26 - 35	50 - 66	99 - 113	PFYD TLTSYVLRSD (SEQ ID NO: 2243)
I087F09	76	140 - 250	165 - 176	192 - 198	231 - 239	1 - 124	26 - 35	50 - 66	99 - 113	PFYD TLTSYVPLPP (SEQ ID NO: 2310)
I087G05	77	140 - 250	165 - 176	192 - 198	231 - 239	1 - 124	26 - 35	50 - 66	99 - 113	PFYD TLTSYVLRCLV (SEQ ID NO: 2239)
I087G06	78	140 - 250	165 - 176	192 - 198	231 - 239	1 - 124	26 - 35	50 - 66	99 - 113	PFYD TLTSYVHPSRS (SEQ ID NO: 2285)
I087G07	79	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVLRPLPPQ (SEQ ID NO: 2241)
I087G09	80	140 - 250	165 - 176	192 - 198	231 - 239	1 - 124	26 - 35	50 - 66	99 - 113	PFYD TLTSYVGPYGT (SEQ ID NO: 2284)
I087G10	81	140 - 250	165 - 176	192 - 198	231 - 239	1 - 124	26 - 35	50 - 66	99 - 113	PFYD TLTSYVTPCT (SEQ ID NO: 2276)
I087H02	82	137 - 244	160 - 170	186 - 192	225 - 233	1 - 121	26 - 35	50 - 66	99 - 110	ASYLSTSSLDN (SEQ ID NO: 2265)
I088A01	83	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVFQYFDH (SEQ ID NO: 2137)
I088A03	84	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVPLPL (SEQ ID NO: 2290)
I088A04	85	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVHLHYPH (SEQ ID NO: 2335)
I088A08	86	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVFEVYAS (SEQ ID NO: 2323)
I088A09	87	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVILYLLH (SEQ ID NO: 2295)
I088A10	88	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVFQYFDH (SEQ ID NO: 2137)
I088A11	89	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVLMYFPH (SEQ ID NO: 2220)
I088A12	90	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVLFYPL (SEQ ID NO: 2325)
I088B01	91	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVFQYFDH (SEQ ID NO: 2137)
I088B02	92	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVFDDYAS (SEQ ID NO: 2244)
I088B03	93	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVPLPL (SEQ ID NO: 2290)
I088B05	94	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVFQYFDH (SEQ ID NO: 2137)
I088B06	95	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVFQYFDH (SEQ ID NO: 2324)
I088B07	96	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVFQYFDH (SEQ ID NO: 2137)
I088B08	97	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVFQYFDH (SEQ ID NO: 2137)
I088B09	98	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVLEFYLL (SEQ ID NO: 2303)
I088B10	99	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVFQYFDH (SEQ ID NO: 2137)
I088B12	100	140 - 250	165 - 176	192 - 198	231 - 239	1 - 124	26 - 35	50 - 66	99 - 113	PFYD TLTSYVPLDS (SEQ ID NO: 2223)
I088C01	101	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVLYFYP (SEQ ID NO: 2317)

I088C03	102	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I088C09	103	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I088C12	104	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I088D01	105	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I088D03	106	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV LHYAL (SEQ ID NO: 2215)
I088D04	107	140 - 250	165 - 176	192 - 198	231 - 239	1 - 124	26 - 35	50 - 66	99 - 113	PFYD TLTSYV LPPSV (SEQ ID NO: 2225)
I088D07	108	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I088D08	109	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I088D11	110	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I088E01	111	138 - 248	163 - 174	190 - 196	229 - 237	1 - 122	23 - 32	47 - 63	96 - 111	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I088E02	112	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV LHYLY (SEQ ID NO: 2216)
I088E03	113	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I088E04	114	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I088E08	115	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I088E10	116	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I088E11	117	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I088F07	118	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I088G02	119	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I088G03	120	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I088G07	121	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FHYPL (SEQ ID NO: 2260)
I088G09	122	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FPPVYL (SEQ ID NO: 2264)
I088G10	123	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV LHFIDH (SEQ ID NO: 2301)
I088H05	124	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I088H07	125	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I092A03	126	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I092A05	127	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FHYDV (SEQ ID NO: 2258)
I092A06	128	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I092A08	129	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV HEFFSL (SEQ ID NO: 2283)
I092A10	130	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I092A11	131	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I092B01	132	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I092B02	133	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I092B04	134	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I092B05	135	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I092B10	136	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I092B12	137	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)

I092C01	138	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I092C02	139	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I092C07	140	140 - 250	165 - 176	192 - 198	231 - 239	1 - 124	26 - 35	50 - 66	99 - 113	PFYD TLTSYV LALDL (SEQ ID NO: 2328)
I092C08	141	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FGYSL (SEQ ID NO: 2254)
I092C12	142	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I092D01	143	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV LKYYTD (SEQ ID NO: 2226)
I092D07	144	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I092D09	145	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV MHAYPL (SEQ ID NO: 2255)
I092D10	146	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FHYLPV (SEQ ID NO: 2256)
I092D11	147	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I092E01	148	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I092E03	149	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV AFQYFDH (SEQ ID NO: 2230)
I092E04	150	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FEYSV (SEQ ID NO: 2248)
I092E07	151	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I092E10	152	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV LFYYP L (SEQ ID NO: 2327)
I092E11	153	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I092F01	154	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I092F02	155	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I092F05	156	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I092F07	157	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I092F08	158	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I092F11	159	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I092F12	160	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV LAYYPD (SEQ ID NO: 2306)
I092G01	161	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I092G05	162	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I092G10	163	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I092H01	164	137 - 244	160 - 170	186 - 192	225 - 233	1 - 121	26 - 35	50 - 66	99 - 110	ASYLSTSSSLDN (SEQ ID NO: 2265)
I093A06	165	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV L P VYDH (SEQ ID NO: 2334)
I093A09	166	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFAH (SEQ ID NO: 2268)
I093A11	167	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I093A12	168	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I093B02	169	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I093B05	170	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I093B06	171	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I093B09	172	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV LEVYHP (SEQ ID NO: 2318)
I093B12	173	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FAPLVT (SEQ ID NO: 2242)

I093C02	174	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVVLHAYAF (SEQ ID NO: 2332)
I093C03	175	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVVFQYFDH (SEQ ID NO: 2137)
I093C05	176	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVVLYYLH (SEQ ID NO: 2295)
I093D05	177	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVFEFLPL (SEQ ID NO: 2245)
I093D08	178	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVVRPFYAH (SEQ ID NO: 2273)
I093D10	179	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVVFQYFDH (SEQ ID NO: 2137)
I093D12	180	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVVLHFYRV (SEQ ID NO: 2302)
I093E01	181	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVVFQYFDH (SEQ ID NO: 2137)
I093E02	182	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVVIQYFDH (SEQ ID NO: 2297)
I093E05	183	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVHEFSL (SEQ ID NO: 2283)
I093E08	184	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVMQFFPT (SEQ ID NO: 2321)
I093E10	185	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVLSFPV (SEQ ID NO: 2246)
I093F01	186	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVLYYAF (SEQ ID NO: 2251)
I093F03	187	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVVFQYFDH (SEQ ID NO: 2137)
I093F05	188	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVVFQYFDH (SEQ ID NO: 2137)
I093F08	189	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVVFQYFDH (SEQ ID NO: 2137)
I093F11	190	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVVLHFYPL (SEQ ID NO: 2137)
I093G07	191	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVVLQYVVL (SEQ ID NO: 2237)
I093G11	192	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVVFQYFDH (SEQ ID NO: 2137)
I093G12	193	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVVFQYFDH (SEQ ID NO: 2137)
I093H06	194	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVVFQYFDH (SEQ ID NO: 2137)
I094A08	195	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVVFQYFDY (SEQ ID NO: 2280)
I094B07	196	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVLPVWVS (SEQ ID NO: 2228)
I094B08	197	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVVFQYFDH (SEQ ID NO: 2137)
I094B12	198	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVVFQYFDH (SEQ ID NO: 2137)
I094C11	199	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVVFQYFDH (SEQ ID NO: 2137)
I094C12	200	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVVFQYFDH (SEQ ID NO: 2137)
I094D06	201	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVIEYYPV (SEQ ID NO: 2288)
I094D07	202	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVVFQYFDH (SEQ ID NO: 2137)
I094D08	203	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVVLHLYPL (SEQ ID NO: 2314)
I094D09	204	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVVFQYFDH (SEQ ID NO: 2137)
I094D10	205	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVVFQYFDH (SEQ ID NO: 2137)
I094D11	206	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVVFHFYRV (SEQ ID NO: 2218)
I094E04	207	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVVFQYFDH (SEQ ID NO: 2137)
I094E08	208	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVLEAFSL (SEQ ID NO: 2311)
I094F04	209	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYVFGFYPF (SEQ ID NO: 2252)

I094F05	210	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTSYVVFQYFDH (SEQ ID NO: 2137)
I094F10	211	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PIYDILTSYVVFQYFDH (SEQ ID NO: 2278)
I094F11	212	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTSYVVLWYYQD (SEQ ID NO: 2249)
I094F12	213	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTSYVVPFYPL (SEQ ID NO: 2296)
I094G06	214	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTSYVVFQYFDH (SEQ ID NO: 2137)
I094G10	215	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTSYVVFQYFDH (SEQ ID NO: 2137)
I095A04	216	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTSYVVFQYFDH (SEQ ID NO: 2137)
I095A12	217	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTSYVLEVFPL (SEQ ID NO: 2320)
I095B04	218	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTSYVLEFFPA (SEQ ID NO: 2312)
I095B09	219	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTSYVIEYLP (SEQ ID NO: 2287)
I095B10	220	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTSYVHLHYSA (SEQ ID NO: 2217)
I095C02	221	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTSYVLFYYTA (SEQ ID NO: 2331)
I095C05	222	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTSYVHLHLPV (SEQ ID NO: 2337)
I095C07	223	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTSYVVFQYFDH (SEQ ID NO: 2137)
I095C08	224	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTSYVVFQYFDH (SEQ ID NO: 2137)
I095C09	225	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTSYVVMHYPT (SEQ ID NO: 2259)
I095D01	226	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTSYVVFQYFDH (SEQ ID NO: 2137)
I095D02	227	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTSYVVLQYFRY (SEQ ID NO: 2235)
I095D03	228	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTSYVVLQVFDT (SEQ ID NO: 2233)
I095D05	229	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTSYVVFQYFDH (SEQ ID NO: 2137)
I095D09	230	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTSYVVFQYFDH (SEQ ID NO: 2137)
I095E01	231	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTSYVLDYYSS (SEQ ID NO: 2309)
I095E05	232	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDALTSYVVFQYFDH (SEQ ID NO: 2221)
I095E12	233	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTSYVVFQYFDH (SEQ ID NO: 2137)
I095F06	234	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTSYVFPFYPH (SEQ ID NO: 2262)
I095F09	235	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTSYVIGFYPV (SEQ ID NO: 2291)
I095G06	236	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTSYVVFQYFDH (SEQ ID NO: 2137)
I095G09	237	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTSYVMDFYSV (SEQ ID NO: 2253)
I095G11	238	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTSYVVFQYFDH (SEQ ID NO: 2137)
I096A01	239	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTSYVVFQYFDH (SEQ ID NO: 2137)
I096A10	240	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTSYVLPFYAL (SEQ ID NO: 2222)
I096B01	241	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTSYVVFQYFDH (SEQ ID NO: 2137)
I096B03	242	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTSYVVFQYFDH (SEQ ID NO: 2137)
I096C01	243	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTSYVVFQYFDH (SEQ ID NO: 2137)
I096C06	244	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTSYVLPYLTH (SEQ ID NO: 2229)
I096C09	245	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDILTSYVVFQYFDH (SEQ ID NO: 2137)

I096D01	246	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDTLTSYVVFQYFDH (SEQ ID NO: 2137)
I096D02	247	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDTLTSYVVFQYFDH (SEQ ID NO: 2137)
I096D05	248	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDTLTSYVVFQYFDH (SEQ ID NO: 2137)
I096D06	249	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDTLTSYVVFQYFDH (SEQ ID NO: 2137)
I096D09	250	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDTLTSYVVFQYFDH (SEQ ID NO: 2137)
I096E02	251	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDTLTSYVVLGFYPV (SEQ ID NO: 2329)
I096E06	252	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDTLTSYVVLHYHTH (SEQ ID NO: 2336)
I096E11	253	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDTLTSYVVFQYFDH (SEQ ID NO: 2137)
I096F02	254	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDTLTSYVVIHFLPL (SEQ ID NO: 2330)
I096G01	255	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDTLTSYVVPFLPL (SEQ ID NO: 2290)
I096G02	256	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDTLTSYVVFQYFDH (SEQ ID NO: 2137)
I096G05	257	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDTLTSYVVFQYFDH (SEQ ID NO: 2137)
I096G07	258	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDTLTSYVVFQYFDH (SEQ ID NO: 2137)
I096G09	259	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDTLTSYVVMHYLPV (SEQ ID NO: 2257)
I096G12	260	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDTLTSYVLEFFSH (SEQ ID NO: 2315)
I096H01	261	137 - 244	160 - 170	186 - 192	225 - 233	1 - 121	26 - 35	50 - 66	99 - 110	ASYLSTSSSLDN (SEQ ID NO: 2265)
I097A04	262	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDTLTSYVVIHLYVT (SEQ ID NO: 2294)
I097A06	263	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDTLTSYVILPYTIL (SEQ ID NO: 2231)
I097A09	264	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDTLTSYVILHYPI (SEQ ID NO: 2298)
I097B02	265	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDTLTSYVILWFYPL (SEQ ID NO: 2247)
I097B09	266	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDTLTSYVVFQYFDH (SEQ ID NO: 2137)
I097B10	267	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDTLTSYVVFQYFDH (SEQ ID NO: 2137)
I097B11	268	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDTLTSYVVFQYFDH (SEQ ID NO: 2137)
I097C05	269	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDTLTSYVILHYTH (SEQ ID NO: 2219)
I097C09	270	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDTLTSYVILHYAY (SEQ ID NO: 2316)
I097C11	271	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDTLTSYVVFQYFDH (SEQ ID NO: 2137)
I097D05	272	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDTLTSYVVIHFSYL (SEQ ID NO: 2293)
I097D06	273	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDTLTSYVVFQYFDH (SEQ ID NO: 2300)
I097E01	274	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDTLTSYVVFQYFDH (SEQ ID NO: 2137)
I097E04	275	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDTLTSYVVFQYFDH (SEQ ID NO: 2137)
I097E08	276	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDTLTSYVVFQYFDH (SEQ ID NO: 2137)
I097E09	277	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDTLTSYVVFQYFDH (SEQ ID NO: 2137)
I097F09	278	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDTLTSYVVFQYFDH (SEQ ID NO: 2137)
I097G10	279	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDTLTSYVVFQYFAH (SEQ ID NO: 2268)
I097H02	280	137 - 244	160 - 170	186 - 192	225 - 233	1 - 121	26 - 35	50 - 66	99 - 110	ASYLSTSSSLDN (SEQ ID NO: 2265)
I098A04	281	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDTLTSYVVFQYFDH (SEQ ID NO: 2137)

I098A05	282	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I098B08	283	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV LDFYSV (SEQ ID NO: 2308)
I098C01	284	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PIYD TLTSYV FQYFDH (SEQ ID NO: 2278)
I098C04	285	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV LYVAF (SEQ ID NO: 2251)
I098F11	286	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I098F12	287	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FFFYPF (SEQ ID NO: 2250)
I098G02	288	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I098G12	289	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I098H05	290	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I101A01	291	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I101B04	292	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I101B06	293	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV PFLTH (SEQ ID NO: 2304)
I101D04	294	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV LEFFPD (SEQ ID NO: 2313)
I101D07	295	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I101E09	296	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDR (SEQ ID NO: 2279)
I101E12	297	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I101G02	298	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I101G11	299	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I102C03	300	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I102E09	301	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I102F02	302	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I102G08	303	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I102G09	304	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV LHYAH (SEQ ID NO: 2214)
I106A09	305	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I106B02	306	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I106B06	307	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I106C07	308	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I106E05	309	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I106E12	310	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I106G01	311	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I106G03	312	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I106B06	313	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I109D12	314	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I109E12	315	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I109G06	316	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)
I109H04	317	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYD TLTSYV FQYFDH (SEQ ID NO: 2137)

I110B03	318	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDTLTSYVVFQYFDH (SEQ ID NO: 2137)
I112D09	319	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDTLTSYGFQYFDH (SEQ ID NO: 2232)
I112F10	320	141 - 251	166 - 177	193 - 199	232 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PFYDTLTSYVVFQYFDH (SEQ ID NO: 2137)
I089F12	321	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLFPFHGLDS (SEQ ID NO: 2146)
I105E12	322	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLFPHHSFDL (SEQ ID NO: 2147)
I108D08	323	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLFPPLAPLYP (SEQ ID NO: 2148)
I108E06	324	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLFPFHGLDV (SEQ ID NO: 2151)
I113E07	325	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLFPHHSIDL (SEQ ID NO: 2152)
I114G05	326	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLFPHHSFDL (SEQ ID NO: 2147)
I116A01	327	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLFPHHSFDL (SEQ ID NO: 2149)
I116A09	328	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLFPHHSFDL (SEQ ID NO: 2150)
I116C11	329	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLFPHHSFDL (SEQ ID NO: 2147)
I085A01	330	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLFPDHLLF (SEQ ID NO: 2602)
I085A02	331	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLFPSPDLGF (SEQ ID NO: 2639)
I085A03	332	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLFPHTPLSF (SEQ ID NO: 2561)
I085A04	333	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLFPPLAPLFF (SEQ ID NO: 2550)
I085A05	334	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLFPSPDPLSL (SEQ ID NO: 2659)
I085A06	335	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLFPSPAPLSF (SEQ ID NO: 2611)
I085A07	336	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLFPASPLSF (SEQ ID NO: 2390)
I085A09	337	138 - 248	162 - 172	188 - 194	227 - 237	1 - 122	26 - 35	50 - 66	99 - 111	SRDLLFPNDALS (SEQ ID NO: 2632)
I085A10	338	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLFPSPAPLRF (SEQ ID NO: 2609)
I085A11	339	138 - 248	162 - 172	188 - 194	227 - 237	1 - 122	26 - 35	50 - 66	99 - 111	SRDLLFPDPLE (SEQ ID NO: 2363)
I085B01	340	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLFPQSPLYP (SEQ ID NO: 2466)
I085B02	341	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLFPHSSLVF (SEQ ID NO: 2392)
I085B03	342	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLFPYDPLLF (SEQ ID NO: 2638)
I085B04	343	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLFPHAPLYF (SEQ ID NO: 2589)
I085B05	344	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLFPHAPLSP (SEQ ID NO: 2573)
I085B06	345	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLFPLSPLSF (SEQ ID NO: 2574)
I085B07	346	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLFPDFFMAP (SEQ ID NO: 2433)
I085B10	347	138 - 248	162 - 172	188 - 194	227 - 237	1 - 122	26 - 35	50 - 66	99 - 111	SRDLLFPHSPLY (SEQ ID NO: 2470)
I085B12	348	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLFPQDPLSP (SEQ ID NO: 2372)
I085C02	349	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLFPDDPLLS (SEQ ID NO: 2430)
I085C03	350	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLFPHGPLLI (SEQ ID NO: 2400)
I085C05	351	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLFPGPSPLLF (SEQ ID NO: 2491)
I085C06	352	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLFPTAALS (SEQ ID NO: 2341)
I085C07	353	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLFPHTPLRF (SEQ ID NO: 2375)

I085C09	354	138 - 248	162 - 172	188 - 194	227 - 237	1 - 122	26 - 35	50 - 66	99 - 111	SRDLLLLFPHSPLT (SEQ ID NO: 2468)
I085C10	355	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPFSPLLF (SEQ ID NO: 2471)
I085C12	356	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFSPHPLFF (SEQ ID NO: 2680)
I085D01	357	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPRPLLLF (SEQ ID NO: 2548)
I085D02	358	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPSQYLDL (SEQ ID NO: 2523)
I085D03	359	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPSSPLLF (SEQ ID NO: 2713)
I085D04	360	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPYFPLVF (SEQ ID NO: 2646)
I085D06	361	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPGSPLLD (SEQ ID NO: 2488)
I085D07	362	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPQAPLLF (SEQ ID NO: 2694)
I085D08	363	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHSYLSP (SEQ ID NO: 2477)
I085D09	364	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPQTPLFP (SEQ ID NO: 2467)
I085D10	365	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHSPLHP (SEQ ID NO: 2563)
I085D11	366	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHAPLAP (SEQ ID NO: 2510)
I085D12	367	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHHTLRF (SEQ ID NO: 2495)
I085E01	368	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPYAVLHF (SEQ ID NO: 2620)
I085E02	369	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPTSPLRL (SEQ ID NO: 2575)
I085E07	370	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPSDALSF (SEQ ID NO: 2568)
I085E08	371	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPNAPLDP (SEQ ID NO: 2603)
I085E09	372	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHDPPRF (SEQ ID NO: 2628)
I085E10	373	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPSEPLWP (SEQ ID NO: 2668)
I085E11	374	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPSSPLSN (SEQ ID NO: 2716)
I085E12	375	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHLPLTP (SEQ ID NO: 2431)
I085F01	376	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPRSPLLF (SEQ ID NO: 2551)
I085F02	377	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPTSPLQL (SEQ ID NO: 2376)
I085F03	378	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPYTPLLF (SEQ ID NO: 2682)
I085F04	379	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPSSPLAF (SEQ ID NO: 2707)
I085F05	380	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHDPLYF (SEQ ID NO: 2706)
I085F06	381	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPSAHLHF (SEQ ID NO: 2586)
I085F07	382	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPAGPLRF (SEQ ID NO: 2410)
I085F09	383	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPDHAFFV (SEQ ID NO: 2439)
I085F10	384	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPSDSGFA (SEQ ID NO: 2662)
I085F11	385	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPSSYLEF (SEQ ID NO: 2339)
I085F12	386	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPRDPLII (SEQ ID NO: 2558)
I085G01	387	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPSAPLHP (SEQ ID NO: 2605)
I085G02	388	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPNAPLLL (SEQ ID NO: 2613)
I085G03	389	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPAAPLLF (SEQ ID NO: 2403)

I085G04	390	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPSAPLDP (SEQ ID NO: 2601)
I085G07	391	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPNAVLDI (SEQ ID NO: 2629)
I085G08	392	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPSEPLFF (SEQ ID NO: 2664)
I085G09	393	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPSSVLWP (SEQ ID NO: 2338)
I085G10	394	138 - 248	162 - 172	188 - 194	227 - 237	1 - 122	26 - 35	50 - 66	99 - 111	SRDLLLLFPHAPLQ (SEQ ID NO: 2554)
I085G11	395	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPDPLAP (SEQ ID NO: 2445)
I085G12	396	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPSSPLHP (SEQ ID NO: 2576)
I085H10	397	142 - 249	163 - 173	189 - 195	228 - 238	1 - 126	26 - 35	50 - 66	99 - 115	DGYYDILTGYSYGMVDV (SEQ ID NO: 2135)
I086A03	398	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPSMPLTF (SEQ ID NO: 2695)
I086A04	399	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHSILHP (SEQ ID NO: 2438)
I086A05	400	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHAPLSH (SEQ ID NO: 2569)
I086A07	401	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPDAAALRF (SEQ ID NO: 2421)
I086A09	402	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPSSHLSF (SEQ ID NO: 2704)
I086A10	403	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPSAPLSS (SEQ ID NO: 2624)
I086A11	404	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHAPLTP (SEQ ID NO: 2577)
I086A12	405	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPYDPLHS (SEQ ID NO: 2635)
I086B02	406	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHFPLHP (SEQ ID NO: 2348)
I086B03	407	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPAHPLLF (SEQ ID NO: 2412)
I086B05	408	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPFEPLII (SEQ ID NO: 2457)
I086B06	409	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPASPLNP (SEQ ID NO: 2364)
I086B07	410	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPSSPLYF (SEQ ID NO: 2720)
I086B09	411	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPTSPLSF (SEQ ID NO: 2579)
I086B10	412	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPDDGLSS (SEQ ID NO: 2428)
I086B11	413	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPISPLCF (SEQ ID NO: 2530)
I086C03	414	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPTAPLYG (SEQ ID NO: 2535)
I086C05	415	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHSLFF (SEQ ID NO: 2427)
I086C07	416	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPQGPLRF (SEQ ID NO: 2440)
I086C08	417	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPAAPLAF (SEQ ID NO: 2401)
I086C09	418	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHLPLLF (SEQ ID NO: 2350)
I086C10	419	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPTFPLIF (SEQ ID NO: 2541)
I086C11	420	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPDDPLSF (SEQ ID NO: 2432)
I086C12	421	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPTDSLFF (SEQ ID NO: 2622)
I086D01	422	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPSAPLTP (SEQ ID NO: 2630)
I086D04	423	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPYAPLYD (SEQ ID NO: 2697)
I086D05	424	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHSPLSF (SEQ ID NO: 2461)
I086D06	425	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPTAPLDL (SEQ ID NO: 2379)

I086D07	426	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHTHLTF (SEQ ID NO: 2365)
I086D08	427	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHSSLD (SEQ ID NO: 2473)
I086D09	428	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPNHPMFP (SEQ ID NO: 2665)
I086D10	429	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPLSSLEF (SEQ ID NO: 2587)
I086D11	430	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPNAPLHP (SEQ ID NO: 2610)
I086D12	431	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPRAHLRF (SEQ ID NO: 2469)
I086E02	432	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPYDPLHF (SEQ ID NO: 2621)
I086E03	433	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHDALQS (SEQ ID NO: 2598)
I086E05	434	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPRTPPLTF (SEQ ID NO: 2567)
I086E07	435	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPAAHLSF (SEQ ID NO: 2398)
I086E08	436	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPRAPLLF (SEQ ID NO: 2490)
I086E09	437	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPFSPLAP (SEQ ID NO: 2464)
I086E10	438	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPRAPLDF (SEQ ID NO: 2367)
I086E12	439	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPTAPLRF (SEQ ID NO: 2522)
I086F02	440	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPSSPLRI (SEQ ID NO: 2714)
I086F05	441	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPTPLQF (SEQ ID NO: 2540)
I086F08	442	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFSDPLSA (SEQ ID NO: 2643)
I086F09	443	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPYNPPIF (SEQ ID NO: 2653)
I086F11	444	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHTPLLF (SEQ ID NO: 2489)
I086G03	445	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHAPLDL (SEQ ID NO: 2513)
I086G04	446	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPFDPLLI (SEQ ID NO: 2454)
I086G05	447	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPTDALRI (SEQ ID NO: 2537)
I086G06	448	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPAAPLTP (SEQ ID NO: 2407)
I086G07	449	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPEGPLLF (SEQ ID NO: 2448)
I086G09	450	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPYAPLSF (SEQ ID NO: 2385)
I086G10	451	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPADSLSF (SEQ ID NO: 2391)
I086H05	452	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPYSPLTH (SEQ ID NO: 2679)
I089A01	453	138 - 248	162 - 172	188 - 194	227 - 237	1 - 122	26 - 35	50 - 66	99 - 111	SRDLLLLFPHDPLI (SEQ ID NO: 2612)
I089A03	454	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPLTPLLI (SEQ ID NO: 2590)
I089A06	455	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHTPLHF (SEQ ID NO: 2485)
I089A07	456	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPTDALYF (SEQ ID NO: 2539)
I089A08	457	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPYTPLLF (SEQ ID NO: 2682)
I089A10	458	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHQPLTF (SEQ ID NO: 2436)
I089A11	459	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPRTYLDF (SEQ ID NO: 2572)
I089B01	460	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHSPLHS (SEQ ID NO: 2450)
I089B02	461	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHHSFDL (SEQ ID NO: 2147)

I089B03	462	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLFTSPLQP (SEQ ID NO: 2528)
I089B04	463	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLFTTHPLLF (SEQ ID NO: 2556)
I089B05	464	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLFPSSPLIF (SEQ ID NO: 2712)
I089B06	465	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLFPMAPLSP (SEQ ID NO: 2596)
I089B07	466	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLFPYSGLDA (SEQ ID NO: 2374)
I089B08	467	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLFPAAPLSP (SEQ ID NO: 2405)
I089B09	468	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLFPKSPILF (SEQ ID NO: 2384)
I089B10	469	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLFTSPLFF (SEQ ID NO: 2571)
I089B11	470	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLFPNSPLFP (SEQ ID NO: 2388)
I089C01	471	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLFPHYGMDV (SEQ ID NO: 2133)
I089C02	472	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLFPSPILF (SEQ ID NO: 2551)
I089C03	473	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLFPYHPLLF (SEQ ID NO: 2532)
I089C05	474	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLFPSSALRF (SEQ ID NO: 2722)
I089C06	475	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLFPSPYLSF (SEQ ID NO: 2701)
I089C07	476	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLFPQAPLFD (SEQ ID NO: 2683)
I089C09	477	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLFPHPFTF (SEQ ID NO: 2507)
I089D01	478	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLFPHPAPLV (SEQ ID NO: 2581)
I089D02	479	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLFPHYGMDV (SEQ ID NO: 2133)
I089D03	480	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLFPYHPLLF (SEQ ID NO: 2344)
I089D04	481	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLFPSSPLSP (SEQ ID NO: 2717)
I089D05	482	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLFPHPAPLFT (SEQ ID NO: 2546)
I089D07	483	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLFPNDPLLI (SEQ ID NO: 2634)
I089D08	484	138 - 248	162 - 172	188 - 194	227 - 237	1 - 122	26 - 35	50 - 66	99 - 111	SRDLLLFPHPAPLQ (SEQ ID NO: 2554)
I089D09	485	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLFPSPHAFHE (SEQ ID NO: 2677)
I089D11	486	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLFPNHPLYP (SEQ ID NO: 2663)
I089E01	487	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLFPYSPLFP (SEQ ID NO: 2657)
I089E02	488	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLFPQDPLHP (SEQ ID NO: 2346)
I089E03	489	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLFPDAPLFP (SEQ ID NO: 2423)
I089E04	490	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLFPSPPLI (SEQ ID NO: 2453)
I089E06	491	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLFPSPPLF (SEQ ID NO: 2491)
I089E09	492	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLFPSSPLTF (SEQ ID NO: 2718)
I089E10	493	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLFTQPLSF (SEQ ID NO: 2566)
I089E11	494	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLFPPLSPLWP (SEQ ID NO: 2578)
I089F01	495	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLFTFPLLF (SEQ ID NO: 2380)
I089F03	496	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLFPHPDPLLI (SEQ ID NO: 2580)
I089F04	497	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLFPYSPPLF (SEQ ID NO: 2670)

1089F05	498	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHSPLRI (SEQ ID NO: 2459)
1089F06	499	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPRAPLLF (SEQ ID NO: 2490)
1089F08	500	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPRTPPLTF (SEQ ID NO: 2567)
1089F09	501	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPLAPLSF (SEQ ID NO: 2555)
1089F10	502	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPNQPLSF (SEQ ID NO: 2667)
1089F11	503	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPLEPMHF (SEQ ID NO: 2565)
1089G01	504	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPSAPLTF (SEQ ID NO: 2626)
1089G02	505	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFSPHPLLF (SEQ ID NO: 2687)
1089G03	506	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPRTPPLVF (SEQ ID NO: 2721)
1089G05	507	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPGSPLTF (SEQ ID NO: 2389)
1089G06	508	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPTAPLLF (SEQ ID NO: 2514)
1089G07	509	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPSAPLDF (SEQ ID NO: 2597)
1089G08	510	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFSPHPLSF (SEQ ID NO: 2688)
1089G11	511	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPSFPLLF (SEQ ID NO: 2671)
1089H10	512	142 - 249	163 - 173	189 - 195	228 - 238	1 - 126	26 - 35	50 - 66	99 - 115	DGYDILTGYSYYGMDV (SEQ ID NO: 2135)
1090A02	513	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPKPLLF (SEQ ID NO: 2416)
1090A03	514	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPNSTLSF (SEQ ID NO: 2678)
1090A04	515	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPDAPLTP (SEQ ID NO: 2426)
1090A05	516	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHEPLLI (SEQ ID NO: 2648)
1090A06	517	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPTYPLSF (SEQ ID NO: 2600)
1090A07	518	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPTTEPLVL (SEQ ID NO: 2479)
1090A08	519	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPTYPLHF (SEQ ID NO: 2584)
1090B01	520	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHDPLTF (SEQ ID NO: 2627)
1090B03	521	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPQAPLTN (SEQ ID NO: 2705)
1090B04	522	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHAPLEA (SEQ ID NO: 2520)
1090B05	523	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPDHPLLF (SEQ ID NO: 2442)
1090B06	524	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPRAPLSF (SEQ ID NO: 2496)
1090B08	525	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPRGPLRF (SEQ ID NO: 2542)
1090B11	526	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPFTPLTF (SEQ ID NO: 2474)
1090B12	527	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPQHPLSP (SEQ ID NO: 2452)
1090C01	528	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPSAPIVF (SEQ ID NO: 2591)
1090C02	529	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPQAPLTF (SEQ ID NO: 2702)
1090C03	530	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPRAPLRF (SEQ ID NO: 2493)
1090C05	531	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPRTPPLTF (SEQ ID NO: 2567)
1090C06	532	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHAPLDF (SEQ ID NO: 2538)
1090C07	533	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHAGFDS (SEQ ID NO: 2498)

I090C08	534	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPYSPLSF (SEQ ID NO: 2676)
I090C10	535	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPGRLTF (SEQ ID NO: 2358)
I090D02	536	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPAEHLF (SEQ ID NO: 2408)
I090D03	537	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPTAPLHP (SEQ ID NO: 2351)
I090D04	538	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHEPLTA (SEQ ID NO: 2654)
I090D05	539	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHAPLFE (SEQ ID NO: 2529)
I090D06	540	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPRAPLDF (SEQ ID NO: 2367)
I090D07	541	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPFGTLRF (SEQ ID NO: 2462)
I090D08	542	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPSSPLVF (SEQ ID NO: 2723)
I090D09	543	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPRDPLAF (SEQ ID NO: 2505)
I090D12	544	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPTSPLSF (SEQ ID NO: 2579)
I090E04	545	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHAPLLL (SEQ ID NO: 2552)
I090E05	546	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPSAPISF (SEQ ID NO: 2588)
I090E06	547	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPQGPLSF (SEQ ID NO: 2443)
I090E07	548	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPGSPLHP (SEQ ID NO: 2484)
I090E09	549	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFSDPLSF (SEQ ID NO: 2647)
I090E11	550	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHDGLAP (SEQ ID NO: 2700)
I090E12	551	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPTSPLTF (SEQ ID NO: 2582)
I090F01	552	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPNGPLHP (SEQ ID NO: 2649)
I090F02	553	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPQAPLSF (SEQ ID NO: 2696)
I090F03	554	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPTAPLSF (SEQ ID NO: 2526)
I090F04	555	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPPFPLQF (SEQ ID NO: 2460)
I090F05	556	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPLDPLHF (SEQ ID NO: 2359)
I090F06	557	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPSEPLQL (SEQ ID NO: 2666)
I090F07	558	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPFAPLRF (SEQ ID NO: 2451)
I090F08	559	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPLHPLIF (SEQ ID NO: 2570)
I090F09	560	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHYPLLF (SEQ ID NO: 2344)
I090F10	561	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPRDPLRI (SEQ ID NO: 2527)
I090F11	562	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPSNPLTF (SEQ ID NO: 2698)
I090G01	563	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPTAPLEI (SEQ ID NO: 2347)
I090G02	564	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPRDPLQF (SEQ ID NO: 2395)
I090G04	565	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHEPLAF (SEQ ID NO: 2633)
I090G05	566	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPRAPLAF (SEQ ID NO: 2472)
I090G06	567	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPYSPLAF (SEQ ID NO: 2656)
I090G07	568	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFHTPLDS (SEQ ID NO: 2480)
I090G08	569	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFHTPLTF (SEQ ID NO: 2492)

I090G09	570	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPSEPLRI (SEQ ID NO: 2356)
I090G10	571	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPTAPLDF (SEQ ID NO: 2343)
I090G12	572	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPNRGLDL (SEQ ID NO: 2669)
I091A02	573	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPYDPLFM (SEQ ID NO: 2724)
I091A03	574	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHAPLYP (SEQ ID NO: 2592)
I091A06	575	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPSAPLAF (SEQ ID NO: 2594)
I091A11	576	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHSPITF (SEQ ID NO: 2441)
I091B01	577	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPYPLFF (SEQ ID NO: 2585)
I091B02	578	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPYAPLDF (SEQ ID NO: 2361)
I091B04	579	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPRDPLQF (SEQ ID NO: 2395)
I091B05	580	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHAPLEL (SEQ ID NO: 2475)
I091B07	581	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPSAPLTF (SEQ ID NO: 2626)
I091B10	582	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPTAPLAF (SEQ ID NO: 2342)
I091B11	583	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHSPLDF (SEQ ID NO: 2444)
I091B12	584	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPSHPLTF (SEQ ID NO: 2690)
I091C02	585	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPAHPLVI (SEQ ID NO: 2414)
I091C03	586	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPQAPLYP (SEQ ID NO: 2378)
I091C04	587	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPTAPLTF (SEQ ID NO: 2531)
I091C05	588	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPTTPLHF (SEQ ID NO: 2583)
I091C06	589	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHYPLLF (SEQ ID NO: 2344)
I091C09	590	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHHPLSF (SEQ ID NO: 2415)
I091C11	591	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPYHSYDI (SEQ ID NO: 2650)
I091C12	592	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPYATLSF (SEQ ID NO: 2618)
I091D01	593	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPNSPLAP (SEQ ID NO: 2672)
I091D02	594	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPYSPLQP (SEQ ID NO: 2673)
I091D04	595	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPQGPLSF (SEQ ID NO: 2443)
I091D05	596	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHDPLAP (SEQ ID NO: 2606)
I091D06	597	138 - 248	162 - 172	188 - 194	227 - 237	1 - 122	26 - 35	50 - 66	99 - 111	SRDLLLLFPHSPLL (SEQ ID NO: 2456)
I091D07	598	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPNGALRF (SEQ ID NO: 2645)
I091D09	599	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPYSPLRF (SEQ ID NO: 2719)
I091E01	600	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPDAPLHP (SEQ ID NO: 2425)
I091E02	601	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPQAPLFP (SEQ ID NO: 2689)
I091E03	602	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPSAPLWP (SEQ ID NO: 2352)
I091E04	603	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFKSPLAF (SEQ ID NO: 2547)
I091E06	604	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPSPLHP (SEQ ID NO: 2576)
I091E07	605	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPNHPLTF (SEQ ID NO: 2661)

I091E08	606	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPNAPLDS (SEQ ID NO: 2607)
I091E09	607	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPYAPLDF (SEQ ID NO: 2361)
I091E10	608	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPSSPLEF (SEQ ID NO: 2711)
I091F01	609	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPRAPLFF (SEQ ID NO: 2486)
I091F03	610	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPMAPLVG (SEQ ID NO: 2599)
I091F05	611	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPLAPLHP (SEQ ID NO: 2553)
I091F06	612	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHDPLGF (SEQ ID NO: 2353)
I091F07	613	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHYGMDV (SEQ ID NO: 2133)
I091F08	614	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPQSPLLF (SEQ ID NO: 2458)
I091F09	615	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHEHLSF (SEQ ID NO: 2354)
I091F10	616	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHSPLDF (SEQ ID NO: 2444)
I091F11	617	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHSPLSP (SEQ ID NO: 2549)
I091F12	618	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHYGMDV (SEQ ID NO: 2133)
I091G01	619	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPNAALYP (SEQ ID NO: 2386)
I091G03	620	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPNDPLFG (SEQ ID NO: 2355)
I091G04	621	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPGAPLSP (SEQ ID NO: 2478)
I091G05	622	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	ARDLLLLFAAPLWP (SEQ ID NO: 2397)
I091G06	623	138 - 248	162 - 172	188 - 194	227 - 237	1 - 122	26 - 35	50 - 66	99 - 111	SRDLLLLFPNDPLR (SEQ ID NO: 2637)
I091G07	624	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPTAPLDP (SEQ ID NO: 2345)
I091G09	625	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPTAPLFP (SEQ ID NO: 2349)
I091G10	626	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFSDPLVF (SEQ ID NO: 2660)
I091G11	627	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPGSPLTF (SEQ ID NO: 2389)
I091G12	628	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPYSHLEF (SEQ ID NO: 2655)
I104A01	629	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPQSPLHP (SEQ ID NO: 2455)
I104A07	630	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPQAPLFP (SEQ ID NO: 2689)
I104A08	631	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPYAPLTF (SEQ ID NO: 2617)
I104A09	632	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPQNPLHP (SEQ ID NO: 2506)
I104A10	633	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHEPLCF (SEQ ID NO: 2636)
I104A11	634	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPSAPLSF (SEQ ID NO: 2611)
I104A12	635	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPMAPLRF (SEQ ID NO: 2593)
I104B02	636	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPRSPLSF (SEQ ID NO: 2557)
I104B04	637	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPSAPLYP (SEQ ID NO: 2387)
I104B09	638	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPRDPLQF (SEQ ID NO: 2395)
I104B11	639	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPTAPLTF (SEQ ID NO: 2531)
I104C01	640	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPYSPLYP (SEQ ID NO: 2710)
I104C04	641	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPASPLIF (SEQ ID NO: 2417)

I104C05	642	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPRHPLLF (SEQ ID NO: 2543)
I104C06	643	138 - 248	162 - 172	188 - 194	227 - 237	1 - 122	26 - 35	50 - 66	99 - 111	SRDLLLLFPHAPLE (SEQ ID NO: 2524)
I104C07	644	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHAPLHP (SEQ ID NO: 2370)
I104C09	645	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHFPLIF (SEQ ID NO: 2399)
I104C11	646	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHEPLIF (SEQ ID NO: 2644)
I104D01	647	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPNHAFDL (SEQ ID NO: 2652)
I104D02	648	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHITILYP (SEQ ID NO: 2497)
I104D03	649	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPDWPLYP (SEQ ID NO: 2483)
I104D04	650	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLPHYPLFL (SEQ ID NO: 2511)
I104D07	651	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPQAPLHP (SEQ ID NO: 2691)
I104D08	652	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHPMDP (SEQ ID NO: 2595)
I104D09	653	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPRAPLTF (SEQ ID NO: 2500)
I104E01	654	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPRATLEF (SEQ ID NO: 2502)
I104E02	655	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHSPLFP (SEQ ID NO: 2447)
I104E03	656	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPNDPLVL (SEQ ID NO: 2641)
I104E05	657	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHDPLYI (SEQ ID NO: 2463)
I104E11	658	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPYAPLSF (SEQ ID NO: 2385)
I104E12	659	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPASPLNP (SEQ ID NO: 2364)
I104F02	660	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHDPLSP (SEQ ID NO: 2616)
I104F03	661	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPRDPLRF (SEQ ID NO: 2360)
I104F04	662	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPGDPLDF (SEQ ID NO: 2481)
I104F05	663	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHGPLTF (SEQ ID NO: 2402)
I104F06	664	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHAPLSP (SEQ ID NO: 2573)
I104F07	665	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPSSPLIL (SEQ ID NO: 2465)
I104F10	666	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPNSPLSP (SEQ ID NO: 2362)
I104F11	667	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPQDPLVF (SEQ ID NO: 2708)
I104F12	668	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPKAPLVF (SEQ ID NO: 2544)
I104G04	669	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHAPLRF (SEQ ID NO: 2559)
I104G05	670	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPRAPLAP (SEQ ID NO: 2476)
I104G09	671	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPTAPLNF (SEQ ID NO: 2518)
I104G11	672	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPQGPLSF (SEQ ID NO: 2482)
I105A02	673	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHPLNP (SEQ ID NO: 2494)
I105A03	674	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHSFDL (SEQ ID NO: 2147)
I105A04	675	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPGAPLAP (SEQ ID NO: 2487)
I105A08	676	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPQAPLYP (SEQ ID NO: 2378)
I105A09	677	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPRSPLSF (SEQ ID NO: 2557)

I105A11	678	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLPSSHFDI (SEQ ID NO: 2692)
I105B04	679	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLPYSPLHP (SEQ ID NO: 2658)
I105B05	680	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLPYSPLSF (SEQ ID NO: 2676)
I105B07	681	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLPPHSHFDL (SEQ ID NO: 2147)
I105B08	682	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLPPHSHFDL (SEQ ID NO: 2147)
I105B10	683	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLPASHPLNP (SEQ ID NO: 2364)
I105B11	684	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLPHEPLSP (SEQ ID NO: 2651)
I105B12	685	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLPPLDPLII (SEQ ID NO: 2560)
I105C02	686	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLPAPLAF (SEQ ID NO: 2472)
I105C03	687	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLPSSPLSF (SEQ ID NO: 2715)
I105C05	688	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLPHYGMDV (SEQ ID NO: 2133)
I105C06	689	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLPAPLDF (SEQ ID NO: 2367)
I105C08	690	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLPSPPLTF (SEQ ID NO: 2562)
I105C12	691	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLPQHGFD (SEQ ID NO: 2446)
I105D04	692	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLPRDPLRF (SEQ ID NO: 2360)
I105D06	693	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLPRDPLSF (SEQ ID NO: 2368)
I105D08	694	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLPYAPLAF (SEQ ID NO: 2608)
I105D09	695	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLPFAAFDV (SEQ ID NO: 2619)
I105D11	696	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLPHEPLFP (SEQ ID NO: 2640)
I105E01	697	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLPSPALTF (SEQ ID NO: 2519)
I105E06	698	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLPPHSHFDS (SEQ ID NO: 2422)
I105E11	699	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLPHYGMDV (SEQ ID NO: 2133)
I105F03	700	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLPNSPLHP (SEQ ID NO: 2675)
I105F06	701	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLPHHPLDS (SEQ ID NO: 2409)
I105F07	702	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLPQAPLHP (SEQ ID NO: 2691)
I105F09	703	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLPSPWPLTF (SEQ ID NO: 2340)
I105F12	704	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLPHYPLLF (SEQ ID NO: 2344)
I105G03	705	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFTYPLVF (SEQ ID NO: 2604)
I105G08	706	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHAPLHP (SEQ ID NO: 2370)
I105G09	707	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPKHPLVF (SEQ ID NO: 2366)
I105G09	708	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLPASHPLNP (SEQ ID NO: 2364)
I105G10	709	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLPPHSHFDA (SEQ ID NO: 2419)
I105G11	710	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLPHDPLLF (SEQ ID NO: 2614)
I107A01	711	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLPSPALTF (SEQ ID NO: 2545)
I107A03	712	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLPAPLHP (SEQ ID NO: 2501)
I107A06	713	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHAPLDP (SEQ ID NO: 2369)

I107A07	714	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPNAPLSP (SEQ ID NO: 2371)
I107A09	715	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPQAPLSP (SEQ ID NO: 2699)
I107A12	716	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHPAPLSF (SEQ ID NO: 2564)
I107B02	717	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHPAPLFP (SEQ ID NO: 2533)
I107B04	718	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPASPLTF (SEQ ID NO: 2420)
I107B05	719	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHYGMDV (SEQ ID NO: 2133)
I107C01	720	137 - 247	161 - 171	187 - 193	226 - 236	1 - 121	24 - 33	48 - 64	97 - 110	SRDLLLLFPHYPLLF (SEQ ID NO: 2344)
I107C02	721	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHYGMYV (SEQ ID NO: 2504)
I107C04	722	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHYPLHP (SEQ ID NO: 2357)
I107C06	723	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHPAPLAP (SEQ ID NO: 2510)
I107C08	724	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPQAPLEP (SEQ ID NO: 2681)
I107C10	725	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPSSHAFDL (SEQ ID NO: 2674)
I107D01	726	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPYAPLDF (SEQ ID NO: 2361)
I107D04	727	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPNAPLSF (SEQ ID NO: 2625)
I107D07	728	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPSSHFDV (SEQ ID NO: 2693)
I107D12	729	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHHSFDT (SEQ ID NO: 2424)
I107E01	730	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPMGLDL (SEQ ID NO: 2499)
I107E05	731	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPRAPLDF (SEQ ID NO: 2367)
I107E07	732	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPRSPLLF (SEQ ID NO: 2551)
I107E09	733	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPKAPLTF (SEQ ID NO: 2382)
I107F01	734	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPSAPLSP (SEQ ID NO: 2623)
I107F05	735	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHPAPLAP (SEQ ID NO: 2510)
I107F09	736	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPSAPLAP (SEQ ID NO: 2394)
I107F10	737	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPRTPLLF (SEQ ID NO: 2373)
I107G01	738	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPNAPLSP (SEQ ID NO: 2371)
I107G05	739	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPSAPLYP (SEQ ID NO: 2387)
I107H02	740	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHHSFDL (SEQ ID NO: 2147)
I107H06	741	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPRAPLSF (SEQ ID NO: 2496)
I107H09	742	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHYPLEM (SEQ ID NO: 2536)
I107H10	743	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHPAPLAP (SEQ ID NO: 2510)
I108A12	744	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHHSFDL (SEQ ID NO: 2147)
I108B03	745	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPRDPLLF (SEQ ID NO: 2515)
I108B04	746	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPLSPLVP (SEQ ID NO: 2396)
I108C09	747	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHDPLGF (SEQ ID NO: 2353)
I108C11	748	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHHSLLF (SEQ ID NO: 2429)
I108D10	749	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPASPLNP (SEQ ID NO: 2364)

I108D11	750	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPASPLNP (SEQ ID NO: 2364)
I108D12	751	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPSAPLNP (SEQ ID NO: 2709)
I108E01	752	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHHSFDL (SEQ ID NO: 2147)
I108E03	753	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPKHPLRF (SEQ ID NO: 2393)
I108E05	754	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHAPLFP (SEQ ID NO: 2533)
I108E07	755	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHAPLDP (SEQ ID NO: 2369)
I108E08	756	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHYPLLF (SEQ ID NO: 2344)
I108E09	757	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPSAPLSP (SEQ ID NO: 2623)
I108E10	758	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPRDPLDL (SEQ ID NO: 2509)
I108E11	759	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPRDPLEF (SEQ ID NO: 2516)
I108F10	760	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPNAPLSP (SEQ ID NO: 2371)
I108F12	761	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHYPFDA (SEQ ID NO: 2508)
I108G01	762	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPRDPLRF (SEQ ID NO: 2360)
I108G02	763	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPDAPLAP (SEQ ID NO: 2381)
I108G07	764	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPRAPLAP (SEQ ID NO: 2476)
I108G10	765	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHHSLLF (SEQ ID NO: 2429)
I108G11	766	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHHPLTF (SEQ ID NO: 2377)
I108G12	767	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHHPLTF (SEQ ID NO: 2377)
I108H01	768	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPRDPLHF (SEQ ID NO: 2512)
I108H02	769	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPNAPLNP (SEQ ID NO: 2615)
I108H06	770	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHHSFDL (SEQ ID NO: 2147)
I108H08	771	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPASPLNP (SEQ ID NO: 2364)
I111A06	772	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPQAPLHP (SEQ ID NO: 2691)
I111B12	773	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHHSFDL (SEQ ID NO: 2147)
I111C01	774	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPQHGLDL (SEQ ID NO: 2449)
I111D06	775	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPRDPLLF (SEQ ID NO: 2515)
I111E04	776	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHHSFDL (SEQ ID NO: 2147)
I111E10	777	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPQAPLHP (SEQ ID NO: 2691)
I111E11	778	139 - 250	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHYPLLF (SEQ ID NO: 2344)
I111E12	779	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHHSFDL (SEQ ID NO: 2150)
I111F07	780	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPRAPLYP (SEQ ID NO: 2501)
I111G02	781	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPKAPLDF (SEQ ID NO: 2534)
I111H10	782	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPQHGFDA (SEQ ID NO: 2703)
I113A04	783	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFSAPLWP (SEQ ID NO: 2352)
I113A12	784	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFQEPALP (SEQ ID NO: 2434)
I113B06	785	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHHPLEP (SEQ ID NO: 2411)

I113C06	786	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHHGFDA (SEQ ID NO: 2406)
I113G04	787	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHYPLLF (SEQ ID NO: 2344)
I113G05	788	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHYSLLL (SEQ ID NO: 2517)
I113G10	789	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHHPLOF (SEQ ID NO: 2413)
I113G11	790	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHYPLLF (SEQ ID NO: 2344)
I113H06	791	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHYPLLF (SEQ ID NO: 2344)
I113H07	792	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHHSFDL (SEQ ID NO: 2147)
I113H09	793	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHYTLF (SEQ ID NO: 2525)
I114C04	794	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHHGFDA (SEQ ID NO: 2406)
I114C12	795	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPQAPLHP (SEQ ID NO: 2691)
I114D04	796	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHYGMDV (SEQ ID NO: 2133)
I114D06	797	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHHSFDL (SEQ ID NO: 2147)
I114D10	798	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHYSLVL (SEQ ID NO: 2521)
I114E01	799	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFQEPISP (SEQ ID NO: 2435)
I114E02	800	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPQESFSL (SEQ ID NO: 2437)
I114E03	801	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPKAPLTF (SEQ ID NO: 2382)
I114E11	802	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHDSFFL (SEQ ID NO: 2383)
I114H01	803	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHHSFDL (SEQ ID NO: 2147)
I114H06	804	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHHALDV (SEQ ID NO: 2404)
I114H09	805	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHHSFDL (SEQ ID NO: 2147)
I115A02	806	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHHSFDL (SEQ ID NO: 2684)
I115A07	807	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHYPLLF (SEQ ID NO: 2344)
I115B10	808	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHHSFDL (SEQ ID NO: 2147)
I115C05	809	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHHSFDL (SEQ ID NO: 2501)
I115C06	810	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHHSFDL (SEQ ID NO: 2150)
I115C08	811	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHHSFDL (SEQ ID NO: 2147)
I115C12	812	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHHSFDT (SEQ ID NO: 2424)
I115D07	813	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHYPLLF (SEQ ID NO: 2344)
I115E09	814	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHHSFDL (SEQ ID NO: 2418)
I115F06	815	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHYGMDV (SEQ ID NO: 2685)
I115F07	816	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHYPLLF (SEQ ID NO: 2686)
I115F12	817	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHHSFDL (SEQ ID NO: 2150)
I115G04	818	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHHSFDL (SEQ ID NO: 2418)
I115G05	819	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHYPLLF (SEQ ID NO: 2344)
I115G08	820	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHDSFDL (SEQ ID NO: 2631)
I115H04	821	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLLFPHANLSP (SEQ ID NO: 2503)

I115H07	822	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLPHHYPLLF (SEQ ID NO: 2344)
I115H09	823	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLPHHHRFDL (SEQ ID NO: 2418)
I116A07	824	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLPHYEPLRF (SEQ ID NO: 2642)
I116B01	825	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLPHHSFDL (SEQ ID NO: 2147)
I116B12	826	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLPHHSFDL (SEQ ID NO: 2147)
I116C06	827	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLPHHYPLLF (SEQ ID NO: 2344)
I116D07	828	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLPHHHRFDL (SEQ ID NO: 2147)
I116E02	829	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLPHHHRFDL (SEQ ID NO: 2418)
I116E04	830	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLPHHHRFDL (SEQ ID NO: 2147)
I116F02	831	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLPHHHRFDL (SEQ ID NO: 2150)
I116F11	832	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLPHHYPLLF (SEQ ID NO: 2344)
I116G05	833	139 - 249	163 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLPPQAPLSP (SEQ ID NO: 2699)
I001C09	834	143 - 250	164 - 174	190 - 196	229 - 239	1 - 127	26 - 35	50 - 66	99 - 116	DGSYDILTGYIDNYMDV (SEQ ID NO: 2154)
I006D07	835	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	SHYDILTGLNYYWYFDL (SEQ ID NO: 2166)
I007B03	836	143 - 253	165 - 178	194 - 200	233 - 242	1 - 127	26 - 35	50 - 66	99 - 116	DGSYDILTGYIDNYMDV (SEQ ID NO: 2154)
I007F11	837	140 - 250	162 - 175	191 - 197	230 - 239	1 - 124	26 - 35	50 - 66	99 - 113	DGDILLVPAALMDV (SEQ ID NO: 2160)
I007H08	838	144 - 254	166 - 179	195 - 201	234 - 243	1 - 128	26 - 37	52 - 69	102 - 117	DRYDILTGYYYGMDV (SEQ ID NO: 2129)
I008A09	839	146 - 256	168 - 181	197 - 203	236 - 245	1 - 130	26 - 35	50 - 66	99 - 119	DREAYDILTGYLYYYMDV (SEQ ID NO: 2172)
I008B01	840	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSDGFDI (SEQ ID NO: 2153)
I008C02	841	145 - 255	167 - 180	196 - 202	235 - 244	1 - 129	26 - 37	52 - 67	100 - 118	HVRDYDILTGYRHHYFDY (SEQ ID NO: 2167)
I008C03	842	143 - 250	164 - 174	190 - 196	229 - 239	1 - 127	26 - 35	50 - 65	98 - 116	EGSYDILTGYVGVGRMDV (SEQ ID NO: 2171)
I008C12	843	146 - 256	168 - 181	197 - 203	236 - 245	1 - 130	26 - 35	50 - 68	101 - 119	FNPTYDILTGYVGGYFQH (SEQ ID NO: 2155)
I012A06	844	145 - 254	169 - 179	195 - 201	234 - 243	1 - 129	26 - 37	52 - 67	100 - 118	GRWDYDILTGEHLGYVFDY (SEQ ID NO: 2162)
I016E05	845	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSDGFDI (SEQ ID NO: 2153)
I016F02	846	135 - 245	157 - 170	186 - 192	225 - 234	1 - 119	26 - 35	50 - 66	99 - 108	GMGDHYGMDV (SEQ ID NO: 2161)
I016F04	847	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSDGFDI (SEQ ID NO: 2153)
I016H07	848	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	GYHDPLTSYNNWFDP (SEQ ID NO: 2163)
I018C02	849	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSDGFDI (SEQ ID NO: 2153)
I018C10	850	143 - 250	164 - 174	190 - 196	229 - 239	1 - 127	26 - 35	50 - 66	99 - 116	DGSYDILTGYIDNYMDV (SEQ ID NO: 2154)
I018D07	851	143 - 250	164 - 174	190 - 196	229 - 239	1 - 127	26 - 35	50 - 66	99 - 116	DGSYDILTGYIDNYMDV (SEQ ID NO: 2154)
I018H08	852	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSDGFDI (SEQ ID NO: 2153)
I018H09	853	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSDGFDI (SEQ ID NO: 2153)
I021B05	854	143 - 253	165 - 178	194 - 200	233 - 242	1 - 127	24 - 33	48 - 64	97 - 116	EGGNYDILTGYVIGNGAFDI (SEQ ID NO: 2158)
I022E02	855	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSDGFDI (SEQ ID NO: 2157)
I026E03	856	141 - 251	165 - 175	191 - 197	230 - 240	1 - 125	26 - 35	50 - 66	99 - 114	TDYDILTGYPMGYFDP (SEQ ID NO: 2173)
I027A07	857	144 - 255	167 - 179	195 - 201	234 - 244	1 - 128	26 - 35	50 - 66	99 - 117	GGEYDILTGYVFLGVYDY (SEQ ID NO: 2170)

I003B03	894	140 - 251	163 - 176	192 - 198	231 - 240	1 - 124	26 - 34	49 - 65	98 - 113	ELGSSIVGATTGALDM (SEQ ID NO: 2852)
I003B04	895	138 - 248	162 - 172	188 - 194	227 - 237	1 - 122	25 - 34	49 - 65	98 - 111	RYGDPFYYYMMNV (SEQ ID NO: 2755)
I003B09	896	142 - 249	163 - 173	189 - 195	228 - 238	1 - 126	26 - 35	50 - 66	99 - 115	DGYDILTGYSYGMVDV (SEQ ID NO: 2135)
I003C01	897	140 - 252	164 - 176	192 - 198	231 - 241	1 - 124	26 - 34	49 - 65	98 - 113	ELGSSIVGATTGALDM (SEQ ID NO: 2174)
I003C02	898	141 - 252	164 - 176	192 - 198	231 - 241	1 - 125	26 - 35	50 - 66	99 - 114	GDYDILTGYPACFCQI (SEQ ID NO: 2854)
I003C03	899	141 - 250	164 - 174	190 - 196	229 - 239	1 - 125	26 - 35	50 - 66	99 - 114	GDYDILTGYPACFCQI (SEQ ID NO: 2854)
I003C12	900	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	MEYDILTGYPGGYFDY (SEQ ID NO: 2179)
I003D04	901	139 - 250	162 - 174	190 - 196	229 - 239	1 - 123	26 - 35	50 - 66	99 - 112	RYGDPFYYYMMNV (SEQ ID NO: 2755)
I003E05	902	141 - 253	164 - 176	192 - 198	231 - 242	1 - 125	26 - 35	50 - 66	99 - 114	GDYDILTGYPACFCQI (SEQ ID NO: 2854)
I003F01	903	140 - 251	163 - 176	192 - 198	231 - 240	1 - 124	26 - 34	49 - 65	98 - 113	ELGSSIVGATTGALDM (SEQ ID NO: 2852)
I003F02	904	139 - 251	162 - 175	191 - 197	230 - 240	1 - 123	26 - 35	50 - 66	99 - 112	RYGDPFYYYMMNV (SEQ ID NO: 2755)
I003G01	905	143 - 254	168 - 179	195 - 201	234 - 243	1 - 127	26 - 35	50 - 66	99 - 116	GTGYDILTGYYMGSAFDQ (SEQ ID NO: 2800)
I003G05	906	143 - 255	166 - 179	195 - 201	234 - 244	1 - 127	26 - 35	50 - 66	99 - 116	GSYDILTGFTGSPLDY (SEQ ID NO: 2766)
I003G06	907	145 - 256	168 - 181	197 - 203	236 - 245	1 - 129	26 - 35	50 - 66	99 - 118	DRGNYDILTGYYFHGVDV (SEQ ID NO: 2914)
I003G11	908	144 - 251	165 - 175	191 - 197	230 - 240	1 - 128	26 - 35	50 - 66	99 - 117	DAQSYDILTGYSYAFDI (SEQ ID NO: 2183)
I003H02	909	140 - 253	164 - 176	192 - 198	233 - 242	1 - 124	26 - 35	50 - 66	99 - 113	DNYDILTGYSRRFDP (SEQ ID NO: 2942)
I003H05	910	140 - 251	163 - 176	192 - 198	231 - 240	1 - 124	26 - 34	49 - 65	98 - 113	ELGSSIVGATTGALDM (SEQ ID NO: 2852)
I003H08	911	142 - 249	163 - 173	189 - 195	228 - 238	1 - 126	26 - 35	50 - 66	99 - 115	DGYDILTGYSYGMVDV (SEQ ID NO: 2135)
I005A01	912	141 - 249	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	SHYDILTGLNYWYFDL (SEQ ID NO: 2166)
I005A02	913	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	EGRDILTGYYVYGLDV (SEQ ID NO: 2893)
I005B01	914	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	SHYDILTGLNYWYFDL (SEQ ID NO: 2166)
I005B09	915	137 - 247	159 - 172	188 - 194	227 - 236	1 - 121	26 - 35	50 - 65	98 - 110	TYVDILTGRFFDI (SEQ ID NO: 2866)
I005C01	916	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	SHYDILTGLNYWYFDL (SEQ ID NO: 2166)
I005D02	917	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	DLRYDILTGYPHDAFDI (SEQ ID NO: 2890)
I005D03	918	142 - 249	165 - 175	191 - 197	230 - 238	1 - 126	26 - 35	50 - 66	99 - 115	GAYYDILTGYPYGMVDV (SEQ ID NO: 2860)
I005E01	919	142 - 249	165 - 175	191 - 197	230 - 238	1 - 126	26 - 35	50 - 66	99 - 115	GTYYDILTGYPHYGMVDV (SEQ ID NO: 2774)
I005E08	920	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	SHYDILTGLNYWYFDL (SEQ ID NO: 2166)
I005F01	921	140 - 248	164 - 174	190 - 196	229 - 238	1 - 124	26 - 35	50 - 66	99 - 113	DQHDILTGVYYGMVDV (SEQ ID NO: 2921)
I005F02	922	144 - 251	167 - 177	193 - 199	232 - 240	1 - 128	26 - 35	50 - 66	99 - 117	VSPSYDILTGYYLPHAFDV (SEQ ID NO: 2849)
I005F04	923	137 - 247	159 - 172	188 - 194	227 - 236	1 - 121	26 - 35	50 - 65	98 - 110	TYVDILTGRFFDI (SEQ ID NO: 2866)
I005F08	924	140 - 247	161 - 171	187 - 193	226 - 236	1 - 124	26 - 35	50 - 66	99 - 113	PSYDILTGYYLYFDY (SEQ ID NO: 2850)
I005G01	925	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	DLRYDILTGYPHDAFDI (SEQ ID NO: 2890)
I005G08	926	142 - 249	165 - 175	191 - 197	230 - 238	1 - 126	26 - 35	50 - 66	99 - 115	GAYYDILTGYPYGMVDV (SEQ ID NO: 2860)
I005H02	927	140 - 247	161 - 171	187 - 193	226 - 236	1 - 124	26 - 35	50 - 66	99 - 113	GQYYDILTGYNWFDP (SEQ ID NO: 2857)
I006B01	928	139 - 246	160 - 170	186 - 192	225 - 235	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLFPHYGMVDV (SEQ ID NO: 2133)
I006C09	929	143 - 253	165 - 177	193 - 199	232 - 242	1 - 127	26 - 35	50 - 66	99 - 116	GGYSSGWLRRGGPYNWFDP (SEQ ID NO: 2967)

I006D09	930	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	GDYDILTGYITPLRDY (SEQ ID NO: 2792)
I006E01	931	143 - 253	165 - 178	194 - 200	233 - 242	1 - 127	26 - 35	50 - 68	101 - 116	NLFVWTLPPYYMDV (SEQ ID NO: 2965)
I006E07	932	143 - 250	166 - 176	192 - 198	231 - 239	1 - 127	26 - 35	50 - 66	99 - 116	ADYDILTGYSPITYGMDV (SEQ ID NO: 2762)
I006F01	933	140 - 250	162 - 175	191 - 197	230 - 239	1 - 124	26 - 35	50 - 68	101 - 113	MYDILTGHNFYD (SEQ ID NO: 2879)
I006F02	934	142 - 253	164 - 176	192 - 198	231 - 242	1 - 126	26 - 35	50 - 66	99 - 115	VSRDILTGNVYYYGMDV (SEQ ID NO: 2817)
I006F07	935	143 - 253	165 - 177	193 - 199	232 - 242	1 - 127	26 - 35	50 - 66	99 - 116	GGYSSGWLGRGPNWFDP (SEQ ID NO: 2967)
I006G01	936	146 - 253	169 - 179	195 - 201	234 - 242	1 - 130	26 - 35	50 - 68	101 - 119	AGGYDILTGRDYYYGMDV (SEQ ID NO: 2877)
I006G04	937	132 - 239	153 - 163	179 - 185	218 - 228	1 - 116	26 - 35	50 - 66	99 - 105	RRYALDY (SEQ ID NO: 2920)
I006H01	938	146 - 253	167 - 177	193 - 199	232 - 242	1 - 130	26 - 35	50 - 65	98 - 119	DRGYDILTGYITPHYYGMDV (SEQ ID NO: 2761)
I006H02	939	143 - 253	165 - 177	193 - 199	232 - 242	1 - 127	26 - 35	50 - 66	99 - 116	GGYSSGWLGRGPNWFDP (SEQ ID NO: 2967)
I007A01	940	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDFDI (SEQ ID NO: 2153)
I007A08	941	139 - 249	161 - 174	190 - 196	229 - 238	1 - 123	26 - 35	50 - 66	99 - 114	SHYDILTGLNYWYFDY (SEQ ID NO: 2746)
I007A11	942	140 - 250	162 - 175	191 - 197	230 - 239	1 - 124	26 - 35	50 - 66	99 - 113	ENYDILTGYYGAFDI (SEQ ID NO: 2772)
I007A12	943	144 - 251	165 - 175	191 - 197	230 - 240	1 - 128	26 - 35	50 - 68	101 - 117	GIYDPLTGYSFDFDI (SEQ ID NO: 2892)
I007B04	944	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDFDI (SEQ ID NO: 2153)
I007C04	945	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDFDI (SEQ ID NO: 2153)
I007C08	946	142 - 249	163 - 173	189 - 195	228 - 238	1 - 126	26 - 35	50 - 65	98 - 115	IRLYCYSLTGYPYGMDD (SEQ ID NO: 2810)
I007C12	947	140 - 250	162 - 175	191 - 197	230 - 239	1 - 124	26 - 35	50 - 66	99 - 113	TNYDILTGYQQVDY (SEQ ID NO: 2782)
I007D07	948	140 - 247	161 - 171	187 - 193	226 - 236	1 - 124	26 - 35	50 - 66	99 - 113	GQYDILTGYNWFDP (SEQ ID NO: 2857)
I007D08	949	144 - 251	165 - 175	191 - 197	230 - 240	1 - 128	26 - 35	50 - 68	101 - 117	GIYDILTGYHWDADFID (SEQ ID NO: 2872)
I007E03	950	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDFDI (SEQ ID NO: 2153)
I007E10	951	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	DFYDILTGYPLGMDV (SEQ ID NO: 2741)
I007E11	952	144 - 251	165 - 175	191 - 197	230 - 240	1 - 128	26 - 35	50 - 66	99 - 117	DLPYDILTGYSLTSGMDV (SEQ ID NO: 2923)
I007F06	953	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDFDI (SEQ ID NO: 2153)
I007F08	954	143 - 253	165 - 178	194 - 200	233 - 242	1 - 127	26 - 35	50 - 65	98 - 116	GRRYDILTGYVYHHGMDV (SEQ ID NO: 2811)
I007G07	955	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	SHYDILTGLNYWYFDL (SEQ ID NO: 2166)
I007G09	956	142 - 252	164 - 177	193 - 199	232 - 241	1 - 126	26 - 35	50 - 66	99 - 115	DSGGDILTGYMPYFDY (SEQ ID NO: 2847)
I007G10	957	142 - 249	163 - 173	189 - 195	228 - 238	1 - 126	26 - 35	50 - 65	98 - 115	VGLYDILTGYPPSGMDV (SEQ ID NO: 2805)
I007H07	958	147 - 257	169 - 182	198 - 204	237 - 246	1 - 131	26 - 35	50 - 68	101 - 120	SQAHYDILTGYLWSYGMDV (SEQ ID NO: 2875)
I007H11	959	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	ESYDILTGYRHYGMDL (SEQ ID NO: 2891)
I008A02	960	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDFDI (SEQ ID NO: 2153)
I008A05	961	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDFDI (SEQ ID NO: 2153)
I008A06	962	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDFDI (SEQ ID NO: 2153)
I008A07	963	142 - 249	163 - 173	189 - 195	228 - 238	1 - 126	26 - 35	50 - 66	99 - 115	DREYDILTGYLHAFDM (SEQ ID NO: 2960)
I008A12	964	140 - 250	162 - 175	191 - 197	230 - 239	1 - 124	26 - 35	50 - 66	99 - 113	ENYDILTGYYGAFDI (SEQ ID NO: 2772)
I008B02	965	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDFDI (SEQ ID NO: 2153)

I008B04	966	143 - 253	165 - 178	194 - 200	233 - 242	1 - 127	26 - 35	50 - 66	99 - 116	DGSYDILTGYYIDNYMDV (SEQ ID NO: 2154)
I008B05	967	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	DHYDILTGYYYGMDV (SEQ ID NO: 2760)
I008B06	968	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I008B07	969	140 - 247	163 - 173	189 - 195	228 - 236	1 - 124	24 - 33	48 - 64	97 - 113	GRRYDILTGYYKGPLDY (SEQ ID NO: 2902)
I008B10	970	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	AYYDNLTGFLPYGMGV (SEQ ID NO: 2947)
I008B11	971	144 - 254	166 - 179	195 - 201	234 - 243	1 - 128	26 - 35	50 - 66	99 - 117	EGYDILTGFLDYHGMVDV (SEQ ID NO: 2753)
I008C06	972	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I008C08	973	149 - 259	171 - 183	199 - 205	238 - 248	1 - 133	26 - 35	50 - 66	99 - 122	GPRGGPYDILTGYYLSDAFDI (SEQ ID NO: 2729)
I008C09	974	142 - 249	163 - 173	189 - 195	228 - 238	1 - 126	26 - 35	50 - 66	99 - 115	EYYDILTGYPDYPYGMVDV (SEQ ID NO: 2973)
I008D01	975	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I008D02	976	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I008D03	977	144 - 254	166 - 179	195 - 201	234 - 243	1 - 128	26 - 35	50 - 66	99 - 117	EVRYDILLTRSYLAGPLDN (SEQ ID NO: 2751)
I008D04	978	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I008D05	979	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I008D06	980	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I008D07	981	144 - 254	166 - 179	195 - 201	234 - 243	1 - 128	26 - 35	50 - 66	99 - 117	DRGYDILTGYYRGHGMVDV (SEQ ID NO: 2837)
I008D08	982	144 - 251	165 - 175	191 - 197	230 - 240	1 - 128	26 - 35	50 - 66	99 - 117	DLPPYDILTGYSLTSGMDV (SEQ ID NO: 2923)
I008D12	983	144 - 254	166 - 179	195 - 201	234 - 243	1 - 128	26 - 35	50 - 66	99 - 117	EEGFYDILTGYYGPGYFDY (SEQ ID NO: 2974)
I008E01	984	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I008E02	985	137 - 247	159 - 172	188 - 194	227 - 236	1 - 121	20 - 31	46 - 63	96 - 110	EGYDILTGYSKFLDY (SEQ ID NO: 2906)
I008E03	986	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I008E04	987	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I008E08	988	141 - 252	163 - 175	191 - 197	230 - 241	1 - 125	26 - 35	50 - 66	99 - 114	SHYDILTGLNYWYFDL (SEQ ID NO: 2166)
I008E09	989	143 - 253	165 - 178	194 - 200	233 - 242	1 - 127	26 - 35	50 - 66	99 - 116	ERADYDILTGYYFYDMDV (SEQ ID NO: 2833)
I008E12	990	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 37	52 - 67	100 - 114	FRYDILTSYYYGMDV (SEQ ID NO: 2734)
I008F03	991	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I008F06	992	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I008F07	993	143 - 250	164 - 174	190 - 196	229 - 239	1 - 127	26 - 35	50 - 65	98 - 116	GRRYDILTGYYHHHGMVDV (SEQ ID NO: 2811)
I008F08	994	143 - 253	165 - 178	194 - 200	233 - 242	1 - 127	26 - 35	50 - 66	99 - 116	GHYDILTGYYDDYYGMDV (SEQ ID NO: 2844)
I008F09	995	133 - 243	155 - 168	184 - 190	223 - 232	1 - 117	26 - 35	50 - 65	98 - 106	HDILTGFDY (SEQ ID NO: 2904)
I008F10	996	140 - 247	161 - 171	187 - 193	226 - 236	1 - 124	26 - 35	50 - 66	99 - 113	SGYDILTGYYLGMDV (SEQ ID NO: 2934)
I008F11	997	144 - 251	165 - 175	191 - 197	230 - 240	1 - 128	26 - 35	50 - 68	101 - 117	APYDILTGYSDDYYGMDV (SEQ ID NO: 2968)
I008G02	998	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I008G03	999	140 - 247	161 - 171	187 - 193	226 - 236	1 - 124	26 - 35	50 - 66	99 - 113	GDYDPLTGYSFGVDV (SEQ ID NO: 2941)
I008G04	1000	143 - 253	165 - 178	194 - 200	233 - 242	1 - 127	26 - 35	50 - 65	98 - 116	EGSYDILTGYYVGVGRMDV (SEQ ID NO: 2171)
I008G05	1001	144 - 254	166 - 179	195 - 201	234 - 243	1 - 128	26 - 35	50 - 66	99 - 117	DGYDILTGFFYYYGMDV (SEQ ID NO: 2899)

I008G11	1002	136 - 246	158 - 171	187 - 193	226 - 235	1 - 120	26 - 35	50 - 66	99 - 109	AYYDILTGLDY (SEQ ID NO: 2966)
I008G12	1003	143 - 253	165 - 178	194 - 200	233 - 242	1 - 127	26 - 35	50 - 66	99 - 116	DQQYDILTGYYHYGMDV (SEQ ID NO: 2964)
I008H02	1004	141 - 248	164 - 174	190 - 196	229 - 237	1 - 125	26 - 35	50 - 66	99 - 114	DQVDLLMDHNYMDV (SEQ ID NO: 2918)
I008H03	1005	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSGDFDI (SEQ ID NO: 2153)
I008H06	1006	143 - 253	165 - 178	194 - 200	233 - 242	1 - 127	26 - 35	50 - 65	98 - 116	EGSYDILTGYVVGVRMDV (SEQ ID NO: 2171)
I008H09	1007	143 - 253	165 - 178	194 - 200	233 - 242	1 - 127	26 - 35	50 - 66	99 - 116	DQQYDILTGYYHYGMDV (SEQ ID NO: 2964)
I008H11	1008	141 - 248	164 - 174	190 - 196	229 - 237	1 - 125	26 - 35	50 - 66	99 - 114	TKYDILTGYYHYMDV (SEQ ID NO: 2856)
I012B03	1009	140 - 249	163 - 175	191 - 197	230 - 238	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I012B06	1010	140 - 251	163 - 176	192 - 198	231 - 240	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I012B10	1011	140 - 251	163 - 175	191 - 197	230 - 240	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I012C03	1012	142 - 255	165 - 178	194 - 200	233 - 244	1 - 126	26 - 35	50 - 66	99 - 115	TDRFGAKDVTSRWGMDV (SEQ ID NO: 2814)
I012C06	1013	140 - 251	163 - 176	192 - 198	231 - 240	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I012C09	1014	140 - 250	164 - 174	190 - 196	229 - 239	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I012D12	1015	145 - 256	168 - 180	196 - 202	235 - 245	1 - 129	26 - 35	50 - 66	99 - 118	DRGNYDILTGYYFHGV (SEQ ID NO: 2914)
I012E07	1016	140 - 252	164 - 176	192 - 198	231 - 241	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I012E08	1017	139 - 250	162 - 174	190 - 196	229 - 239	1 - 123	26 - 35	50 - 66	99 - 112	RYGDPFYYYMNV (SEQ ID NO: 2755)
I012E09	1018	140 - 247	163 - 173	189 - 195	228 - 236	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I012F05	1019	140 - 249	163 - 173	189 - 195	228 - 238	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I012F12	1020	140 - 251	164 - 176	192 - 198	231 - 240	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I012G03	1021	140 - 252	164 - 176	192 - 198	231 - 241	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I012G05	1022	139 - 250	163 - 173	189 - 195	228 - 239	1 - 123	26 - 35	50 - 66	99 - 112	RYGDPFYYYMNV (SEQ ID NO: 2755)
I012G10	1023	139 - 251	162 - 175	191 - 197	230 - 240	1 - 123	26 - 35	50 - 66	99 - 112	RYGDPFYYYMNV (SEQ ID NO: 2755)
I012H09	1024	140 - 249	163 - 173	189 - 195	228 - 238	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I013A10	1025	147 - 259	170 - 182	198 - 204	237 - 248	1 - 131	26 - 35	50 - 66	99 - 120	SSPKWYDALTGHSYHSAMDV (SEQ ID NO: 2159)
I013A12	1026	147 - 256	171 - 181	197 - 203	236 - 245	1 - 131	26 - 35	50 - 66	99 - 120	SSPKWYDALTGHSYHSAMDV (SEQ ID NO: 2159)
I013B04	1027	147 - 256	172 - 182	198 - 204	237 - 245	1 - 131	26 - 35	50 - 66	99 - 120	SSPKWYDALTGHSYHSAMDV (SEQ ID NO: 2165)
I013B09	1028	147 - 257	171 - 181	197 - 203	236 - 246	1 - 131	26 - 35	50 - 66	99 - 120	SSPKWYDALTGHSYHSAMDV (SEQ ID NO: 2159)
I013C02	1029	147 - 258	170 - 182	198 - 204	237 - 247	1 - 131	26 - 35	50 - 66	99 - 120	SSPKWYDALTGHSYRSAMDV (SEQ ID NO: 2818)
I013C04	1030	137 - 249	161 - 173	189 - 195	228 - 238	1 - 121	26 - 35	50 - 66	99 - 110	GYDSSAFRAFDI (SEQ ID NO: 2136)
I013D02	1031	137 - 248	160 - 173	189 - 195	228 - 237	1 - 121	26 - 35	50 - 66	99 - 110	GYDSSAFRAFDI (SEQ ID NO: 2136)
I013D03	1032	147 - 259	170 - 183	199 - 205	238 - 248	1 - 131	26 - 35	50 - 66	99 - 120	SSPKWYDALTGDSYHSAMDV (SEQ ID NO: 2165)
I013D10	1033	145 - 257	168 - 181	197 - 203	236 - 246	1 - 129	26 - 35	50 - 66	99 - 118	GLRHVTLFGTGRGHFMDV (SEQ ID NO: 2789)
I013E02	1034	147 - 259	170 - 183	199 - 205	238 - 248	1 - 131	26 - 35	50 - 66	99 - 120	GREDTKVKPWRVYHYMDV (SEQ ID NO: 2809)
I013E05	1035	137 - 249	162 - 173	189 - 195	228 - 238	1 - 121	26 - 35	50 - 66	99 - 110	GYDSSAFRAFDI (SEQ ID NO: 2136)
I013E09	1036	147 - 260	170 - 183	199 - 205	238 - 249	1 - 131	26 - 35	50 - 66	99 - 120	SSPKWYDALTGDSYHSAMDV (SEQ ID NO: 2165)
I013F03	1037	137 - 248	160 - 172	188 - 194	227 - 237	1 - 121	26 - 35	50 - 66	99 - 110	GYDSSAFRAFDI (SEQ ID NO: 2136)

I013F04	1038	147 - 258	170 - 182	198 - 204	237 - 247	1 - 131	26 - 35	50 - 66	99 - 120	SSPPKWDYDALTGHSYHSAMDV (SEQ ID NO: 2159)
I013F07	1039	145 - 260	170 - 185	201 - 207	240 - 249	1 - 129	26 - 35	50 - 66	99 - 118	AATTSQHKNYAYFYGMDV (SEQ ID NO: 2131)
I013F09	1040	137 - 248	160 - 172	188 - 194	227 - 237	1 - 121	26 - 35	50 - 66	99 - 110	GYDSSAFRAFDI (SEQ ID NO: 2136)
I013F10	1041	147 - 259	170 - 183	199 - 205	238 - 248	1 - 131	26 - 35	50 - 66	99 - 120	SSPPKWDYDALTGHSYHSAMDV (SEQ ID NO: 2159)
I013H04	1042	147 - 258	170 - 182	198 - 204	237 - 247	1 - 131	26 - 35	50 - 66	99 - 120	SSPPKWDYDALTGHSYHSAMDV (SEQ ID NO: 2159)
I013H07	1043	147 - 259	170 - 183	199 - 205	238 - 248	1 - 131	26 - 35	50 - 66	99 - 120	GGRTDKVKPWDRYHYYYMDV (SEQ ID NO: 2809)
I014A12	1044	143 - 253	165 - 178	194 - 200	233 - 242	1 - 127	24 - 33	48 - 64	97 - 116	EGGNYDLTGYYIGNGAFDI (SEQ ID NO: 2158)
I014C06	1045	141 - 254	164 - 177	193 - 200	233 - 243	1 - 125	26 - 35	50 - 66	99 - 114	GDYDLTGYPAEFCFI (SEQ ID NO: 2854)
I014C10	1046	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I014C12	1047	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I014E06	1048	140 - 252	164 - 176	192 - 198	231 - 241	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I014F02	1049	141 - 251	166 - 176	192 - 198	231 - 240	1 - 125	26 - 37	52 - 67	100 - 114	AGYDLLTGYPFYFDS (SEQ ID NO: 2757)
I016A08	1050	144 - 251	165 - 175	191 - 197	230 - 240	1 - 128	26 - 35	50 - 66	99 - 117	EVRYDLLTRSYLAGPLDN (SEQ ID NO: 2751)
I016A09	1051	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I016C02	1052	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I016C03	1053	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I016C05	1054	148 - 255	169 - 179	195 - 201	234 - 244	1 - 132	26 - 35	50 - 66	99 - 121	VQMDSEYYDLLTGINVGPPYFDY (SEQ ID NO: 2132)
I016C09	1055	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I016C11	1056	148 - 255	169 - 179	195 - 201	234 - 244	1 - 132	26 - 35	50 - 66	99 - 121	VQMDSEYYDLLTGINVGPPYFDY (SEQ ID NO: 2132)
I016D10	1057	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I016D11	1058	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I016E03	1059	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I016E04	1060	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I016F03	1061	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I016F11	1062	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I016G01	1063	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I016G06	1064	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I016G12	1065	148 - 255	169 - 179	195 - 201	234 - 244	1 - 132	26 - 35	50 - 66	99 - 121	VQMDSEYYDLLTGINVGPPYFDY (SEQ ID NO: 2132)
I016H10	1066	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I017A06	1067	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I017A07	1068	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I017A11	1069	140 - 253	162 - 175	191 - 197	233 - 242	1 - 124	25 - 34	49 - 65	98 - 113	ATYDPLTGYSFDGLDI (SEQ ID NO: 2153)
I017E12	1070	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2157)
I017G03	1071	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I017G07	1072	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I017H01	1073	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)

I018A02	1074	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDFDI (SEQ ID NO: 2153)
I018A04	1075	144 - 254	166 - 179	195 - 201	234 - 243	1 - 128	26 - 35	50 - 66	99 - 117	EGSYDILTGYYGVGRMDV (SEQ ID NO: 2171)
I018A05	1076	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDFDI (SEQ ID NO: 2153)
I018A11	1077	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDFDI (SEQ ID NO: 2153)
I018B02	1078	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDFDI (SEQ ID NO: 2153)
I018B08	1079	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDFDI (SEQ ID NO: 2153)
I018C04	1080	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDFDI (SEQ ID NO: 2153)
I018D02	1081	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDFDI (SEQ ID NO: 2153)
I018E06	1082	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDFDI (SEQ ID NO: 2153)
I018E08	1083	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDFDI (SEQ ID NO: 2153)
I018F04	1084	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDFDI (SEQ ID NO: 2153)
I018G06	1085	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDFDI (SEQ ID NO: 2153)
I018H07	1086	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDFDI (SEQ ID NO: 2153)
I019E05	1087	144 - 254	166 - 179	195 - 201	234 - 243	1 - 128	26 - 35	50 - 66	99 - 117	ERHYDILTGQTYGMDV (SEQ ID NO: 2784)
I019F06	1088	144 - 254	166 - 179	195 - 201	234 - 243	1 - 128	26 - 35	50 - 66	99 - 117	ERHYDILTGQTYGMDV (SEQ ID NO: 2784)
I019G12	1089	143 - 253	165 - 178	194 - 200	233 - 242	1 - 127	24 - 33	48 - 64	97 - 116	EGGYDILTGYYIGNGAFDI (SEQ ID NO: 2158)
I020D01	1090	137 - 247	159 - 171	187 - 193	226 - 236	1 - 121	26 - 35	50 - 66	99 - 110	DRETKVGYGMDV (SEQ ID NO: 2945)
I020D05	1091	143 - 253	165 - 178	194 - 200	233 - 242	1 - 127	24 - 33	48 - 64	97 - 116	EGGYDILTGYYIGNGAFDI (SEQ ID NO: 2158)
I020E10	1092	143 - 253	165 - 178	194 - 200	233 - 242	1 - 127	24 - 33	48 - 64	97 - 116	EGGYDILTGYYIGNGAFDI (SEQ ID NO: 2158)
I020G12	1093	143 - 253	165 - 178	194 - 200	233 - 242	1 - 127	24 - 33	48 - 64	97 - 116	EGGYDILTGYYIGNGAFDI (SEQ ID NO: 2158)
I020H06	1094	143 - 253	165 - 178	194 - 200	233 - 242	1 - 127	24 - 33	48 - 64	97 - 116	EGGYDILTGYYIGNGAFDI (SEQ ID NO: 2158)
I020H10	1095	143 - 253	165 - 178	194 - 200	233 - 242	1 - 127	24 - 33	48 - 64	97 - 116	EGGYDILTGYYIGNGAFDI (SEQ ID NO: 2158)
I021A11	1096	143 - 253	165 - 178	194 - 200	233 - 242	1 - 127	24 - 33	48 - 64	97 - 116	EGGYDILTGYYIGNGAFDI (SEQ ID NO: 2158)
I021B01	1097	143 - 253	165 - 178	194 - 200	233 - 242	1 - 127	24 - 33	48 - 64	97 - 116	EGGYDILTGYYIGNGAFDI (SEQ ID NO: 2158)
I021C11	1098	143 - 253	165 - 178	194 - 200	233 - 242	1 - 127	24 - 33	48 - 64	97 - 116	EGGYDILTGYYIGNGAFDI (SEQ ID NO: 2158)
I021D12	1099	137 - 247	159 - 171	187 - 193	226 - 236	1 - 121	26 - 35	50 - 66	99 - 110	DRETKVGYGMDV (SEQ ID NO: 2945)
I021E10	1100	143 - 253	165 - 178	194 - 200	233 - 242	1 - 127	24 - 33	48 - 64	97 - 116	EGGYDILTGYYIGNGAFDI (SEQ ID NO: 2158)
I021G02	1101	143 - 253	165 - 178	194 - 200	233 - 242	1 - 127	24 - 33	48 - 64	97 - 116	EGGYDILTGYYIGNGAFDI (SEQ ID NO: 2158)
I022A08	1102	142 - 249	163 - 173	189 - 195	228 - 238	1 - 126	26 - 35	50 - 66	99 - 115	DGYYDILTGYSYGMVDV (SEQ ID NO: 2135)
I022B01	1103	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDFDI (SEQ ID NO: 2153)
I022B10	1104	141 - 248	164 - 174	190 - 196	229 - 237	1 - 125	26 - 35	50 - 66	99 - 114	MEYDILTGYYGDFDI (SEQ ID NO: 2179)
I022C02	1105	142 - 249	163 - 173	189 - 195	228 - 238	1 - 126	26 - 35	50 - 66	99 - 115	DGYYDILTGYSYGMVDV (SEQ ID NO: 2135)
I022C04	1106	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDFDI (SEQ ID NO: 2153)
I022C08	1107	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDFDI (SEQ ID NO: 2153)
I022D06	1108	142 - 249	163 - 173	189 - 195	228 - 238	1 - 126	26 - 35	50 - 66	99 - 115	DGYYDILTGYSYGMVDV (SEQ ID NO: 2135)
I022E08	1109	142 - 249	163 - 173	189 - 195	228 - 238	1 - 126	26 - 35	50 - 66	99 - 115	ASYDILTGYYKGAFFI (SEQ ID NO: 2855)

I022F01	1110	142 - 249	163 - 173	189 - 195	228 - 238	1 - 126	26 - 35	50 - 66	99 - 115	DGYDILTGYSYGM DV (SEQ ID NO: 2135)
I022F04	1111	142 - 249	163 - 173	189 - 195	228 - 238	1 - 126	26 - 35	50 - 66	99 - 115	DGYDILTGYSYGM DV (SEQ ID NO: 2135)
I022F12	1112	140 - 247	161 - 171	187 - 193	226 - 236	1 - 124	26 - 35	50 - 66	99 - 113	GDYDILTGYYIDV (SEQ ID NO: 2859)
I022G11	1113	142 - 249	163 - 173	189 - 195	228 - 238	1 - 126	26 - 35	50 - 66	99 - 115	DGYDILTGYSYGM DV (SEQ ID NO: 2135)
I023D01	1114	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	SHYDILTGLNWWYFDL (SEQ ID NO: 2166)
I023D04	1115	142 - 249	163 - 173	189 - 195	228 - 238	1 - 126	26 - 35	50 - 66	99 - 115	DGYDILTGYSYGM DV (SEQ ID NO: 2135)
I024B04	1116	140 - 247	161 - 171	187 - 193	226 - 236	1 - 124	26 - 35	50 - 66	99 - 113	VYYDILTGYNLFFDY (SEQ ID NO: 2177)
I024D01	1117	142 - 249	163 - 173	189 - 195	228 - 238	1 - 126	26 - 35	50 - 66	99 - 115	DGYDILTGYSYGM DV (SEQ ID NO: 2135)
I024F06	1118	142 - 249	163 - 173	189 - 195	228 - 238	1 - 126	26 - 35	50 - 66	99 - 115	DGYDILTGYSYGM DV (SEQ ID NO: 2135)
I024H01	1119	142 - 249	163 - 173	189 - 195	228 - 238	1 - 126	26 - 35	50 - 66	99 - 115	DGYDILTGYSYGM DV (SEQ ID NO: 2135)
I024H07	1120	142 - 249	163 - 173	189 - 195	228 - 238	1 - 126	26 - 35	50 - 66	99 - 115	DGYDILTGYSYGM DV (SEQ ID NO: 2135)
I025A01	1121	140 - 251	163 - 176	192 - 198	231 - 240	1 - 124	26 - 34	49 - 65	98 - 113	ELGSSIVGATTGALDM (SEQ ID NO: 2852)
I025A04	1122	140 - 251	163 - 175	191 - 197	230 - 240	1 - 124	26 - 34	49 - 65	98 - 113	ELGSSIVGATTGALDM (SEQ ID NO: 2852)
I025A07	1123	140 - 249	163 - 173	189 - 195	228 - 238	1 - 124	26 - 34	49 - 65	98 - 113	ELGSSIVGATTGALDM (SEQ ID NO: 2852)
I025B01	1124	133 - 244	156 - 168	184 - 190	223 - 233	1 - 117	26 - 35	50 - 66	99 - 106	DQGRYLDL (SEQ ID NO: 2175)
I025B10	1125	140 - 253	164 - 176	192 - 198	233 - 242	1 - 124	26 - 35	50 - 66	99 - 113	DNYDILTGYSRRFDP (SEQ ID NO: 2942)
I025B12	1126	140 - 251	163 - 176	192 - 198	231 - 240	1 - 124	26 - 34	49 - 65	98 - 113	ELGSSIVGATTGALDM (SEQ ID NO: 2852)
I025C07	1127	140 - 251	163 - 176	192 - 198	231 - 240	1 - 124	26 - 34	49 - 65	98 - 113	ELGSSIVGATTGALDM (SEQ ID NO: 2852)
I025D11	1128	140 - 252	164 - 176	192 - 198	231 - 241	1 - 124	26 - 34	49 - 65	98 - 113	ELGSSIVGATTGALDM (SEQ ID NO: 2852)
I025E04	1129	142 - 252	164 - 176	192 - 198	231 - 241	1 - 126	26 - 35	50 - 66	99 - 115	PLGITAVRGAKTDAGI (SEQ ID NO: 2929)
I025E05	1130	140 - 251	163 - 175	191 - 197	230 - 240	1 - 124	26 - 34	49 - 65	98 - 113	ELGSSIVGATTGALDM (SEQ ID NO: 2174)
I025E07	1131	140 - 252	164 - 176	192 - 198	231 - 241	1 - 124	26 - 34	49 - 65	98 - 113	ELGSSIVGATTGALDM (SEQ ID NO: 2174)
I025E10	1132	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDFDI (SEQ ID NO: 2153)
I025F01	1133	139 - 251	162 - 175	191 - 197	230 - 240	1 - 123	26 - 35	50 - 66	99 - 112	RYGDPFYYYMNV (SEQ ID NO: 2755)
I025F08	1134	137 - 248	160 - 172	188 - 194	227 - 237	1 - 121	26 - 35	50 - 66	99 - 110	GGSSQNFYGM DV (SEQ ID NO: 2884)
I025G03	1135	140 - 252	164 - 176	192 - 198	231 - 241	1 - 124	26 - 34	49 - 65	98 - 113	ELGSSIVGATTGALDM (SEQ ID NO: 2174)
I025G08	1136	140 - 254	163 - 176	192 - 198	231 - 243	1 - 124	26 - 34	49 - 65	98 - 113	ELGSSIVGATTGALDM (SEQ ID NO: 2174)
I025H02	1137	144 - 255	167 - 179	195 - 201	234 - 244	1 - 128	26 - 35	50 - 65	98 - 117	AGSGFHDILTGYYKGGYFDY (SEQ ID NO: 2961)
I026A01	1138	141 - 249	165 - 175	191 - 197	230 - 238	1 - 125	26 - 35	50 - 66	99 - 114	GDYDILTGYPAECEFI (SEQ ID NO: 2854)
I026B01	1139	143 - 254	166 - 178	194 - 200	233 - 243	1 - 127	26 - 35	50 - 66	99 - 116	GSVYDILTGYYKSGMGV (SEQ ID NO: 2733)
I026B06	1140	140 - 251	163 - 176	192 - 198	231 - 240	1 - 124	26 - 34	49 - 65	98 - 113	ELGSSIVGATTGALDM (SEQ ID NO: 2852)
I026C06	1141	140 - 251	163 - 176	192 - 198	231 - 240	1 - 124	26 - 34	49 - 65	98 - 113	ELGSSIVGATTGALDM (SEQ ID NO: 2852)
I026C10	1142	138 - 249	161 - 174	190 - 196	229 - 238	1 - 122	26 - 34	49 - 65	98 - 111	RYGDPFYYYMNV (SEQ ID NO: 2755)
I026C11	1143	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDFDI (SEQ ID NO: 2153)
I026D09	1144	139 - 252	162 - 175	191 - 197	230 - 241	1 - 123	26 - 35	50 - 66	99 - 112	RYGDPFYYYMNV (SEQ ID NO: 2755)
I026E04	1145	140 - 252	164 - 176	192 - 198	231 - 241	1 - 124	26 - 34	49 - 65	98 - 113	ELGSSIVGATTGALDM (SEQ ID NO: 2174)

I026E06	1146	140 - 251	163 - 175	191 - 197	230 - 240	1 - 124	26 - 35	50 - 66	99 - 113	GYDDILTGIMALDY (SEQ ID NO: 2821)
I026E09	1147	140 - 251	163 - 176	192 - 198	231 - 240	1 - 124	26 - 34	49 - 65	98 - 113	ELGSSIVGATTGALDM (SEQ ID NO: 2852)
I026F01	1148	140 - 251	163 - 176	192 - 198	231 - 240	1 - 124	26 - 34	49 - 65	98 - 113	ELGSSIVGATTGALDM (SEQ ID NO: 2852)
I026F09	1149	140 - 251	163 - 176	192 - 198	231 - 240	1 - 124	26 - 34	49 - 65	98 - 113	ELGSSIVGATTGALDM (SEQ ID NO: 2852)
I026F12	1150	140 - 256	163 - 176	192 - 202	237 - 245	1 - 124	26 - 34	49 - 65	98 - 113	ELGSSIVGATTGALDM (SEQ ID NO: 2852)
I026G08	1151	140 - 251	163 - 176	192 - 198	231 - 240	1 - 124	26 - 34	49 - 65	98 - 113	ELGSSIVGATTGALDM (SEQ ID NO: 2852)
I026G10	1152	140 - 251	163 - 176	192 - 198	231 - 240	1 - 124	26 - 34	49 - 65	98 - 113	ELGSSIVGATTGALDM (SEQ ID NO: 2852)
I026G11	1153	143 - 255	166 - 179	195 - 201	234 - 244	1 - 127	26 - 35	50 - 66	99 - 116	GTGYDILTGYYMGSAFDQ (SEQ ID NO: 2800)
I026H02	1154	139 - 251	162 - 175	191 - 197	230 - 240	1 - 123	26 - 35	50 - 66	99 - 112	RYGDPFYYYYMNV (SEQ ID NO: 2755)
I026H06	1155	140 - 251	163 - 175	191 - 197	230 - 240	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I026H10	1156	144 - 255	167 - 179	195 - 201	234 - 244	1 - 128	26 - 35	50 - 66	99 - 117	GGEYDILTGYYFGLGVYDY (SEQ ID NO: 2170)
I027A09	1157	140 - 251	163 - 176	192 - 198	231 - 240	1 - 124	26 - 34	49 - 65	98 - 113	ELGSSIVGATTGALDM (SEQ ID NO: 2852)
I027B02	1158	139 - 250	162 - 174	190 - 196	229 - 239	1 - 123	26 - 35	50 - 66	99 - 112	RYGDPFYYYYMNV (SEQ ID NO: 2755)
I027B05	1159	140 - 250	163 - 176	192 - 198	230 - 239	1 - 124	26 - 34	49 - 65	98 - 113	ELGSSIVGATTGALDM (SEQ ID NO: 2852)
I027C08	1160	138 - 249	161 - 174	190 - 196	229 - 238	1 - 122	26 - 34	49 - 63	96 - 111	ELGSSIVGATTGALDM (SEQ ID NO: 2852)
I027D02	1161	141 - 250	164 - 174	190 - 196	229 - 239	1 - 125	26 - 35	50 - 66	99 - 114	DPFGAVPGYYYAMDV (SEQ ID NO: 2826)
I027E03	1162	140 - 251	163 - 176	192 - 198	231 - 241	1 - 124	26 - 34	49 - 65	98 - 113	ELGSSIVGATTGALDM (SEQ ID NO: 2852)
I027E05	1163	140 - 252	164 - 176	192 - 198	231 - 241	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I027F04	1164	144 - 252	167 - 176	192 - 198	231 - 241	1 - 128	26 - 35	50 - 66	99 - 117	GPWYDPLFPSPGRHYGLDV (SEQ ID NO: 2793)
I027F05	1165	140 - 254	163 - 176	192 - 198	231 - 243	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I027F11	1166	140 - 251	163 - 176	192 - 198	231 - 240	1 - 124	26 - 34	49 - 65	98 - 113	ELGSSIVGATTGALDM (SEQ ID NO: 2852)
I027G06	1167	140 - 253	164 - 176	192 - 198	233 - 242	1 - 124	26 - 35	50 - 66	99 - 113	DNYYDILTGYSRRFDP (SEQ ID NO: 2942)
I027G07	1168	140 - 250	164 - 174	190 - 196	229 - 239	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I027H03	1169	141 - 252	164 - 176	192 - 198	231 - 241	1 - 125	26 - 35	50 - 66	99 - 114	GDYDILTGYPACFQI (SEQ ID NO: 2854)
I028A04	1170	143 - 250	164 - 174	190 - 196	229 - 239	1 - 127	26 - 35	50 - 66	99 - 116	DMYYDILTGYYTGLAFDM (SEQ ID NO: 2880)
I028A07	1171	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	VLNYDILTGYYYGMDV (SEQ ID NO: 2832)
I028B08	1172	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGEDI (SEQ ID NO: 2153)
I028B10	1173	148 - 258	170 - 183	199 - 205	238 - 247	1 - 132	26 - 35	50 - 68	101 - 121	DFGYDILTGYYIGAFYAFDI (SEQ ID NO: 2861)
I028C01	1174	142 - 250	165 - 175	191 - 197	230 - 239	1 - 126	26 - 37	52 - 69	102 - 115	GGHTCIPTCHMGG (SEQ ID NO: 2796)
I028C04	1175	143 - 253	165 - 178	194 - 200	233 - 242	1 - 127	26 - 35	50 - 66	99 - 116	DMYYDILTGYYTGLAFDM (SEQ ID NO: 2880)
I028C08	1176	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGEDI (SEQ ID NO: 2153)
I028D04	1177	140 - 247	163 - 173	189 - 195	228 - 236	1 - 124	26 - 35	50 - 65	98 - 113	ATQDILTGYSFGMDV (SEQ ID NO: 2977)
I028D05	1178	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	EHYDILTGYSLLGMDV (SEQ ID NO: 2907)
I028D12	1179	143 - 250	164 - 174	190 - 196	229 - 239	1 - 127	26 - 35	50 - 66	99 - 116	DGYDILTGYSVYYGMDV (SEQ ID NO: 2938)
I028E06	1180	143 - 253	165 - 178	194 - 200	233 - 242	1 - 127	26 - 35	50 - 65	98 - 116	EGSYDILTGYYVGVGRMDV (SEQ ID NO: 2171)
I028E07	1181	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGEDI (SEQ ID NO: 2153)

I030E05	1218	140 - 252	164 - 176	192 - 198	231 - 241	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I030E07	1219	140 - 251	165 - 176	192 - 198	231 - 240	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I030E08	1220	140 - 251	163 - 175	191 - 197	230 - 240	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I030E09	1221	140 - 252	163 - 176	192 - 198	231 - 241	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I030E10	1222	139 - 250	162 - 174	190 - 196	229 - 239	1 - 123	26 - 35	50 - 66	99 - 112	RYGDPFYYYMMNV (SEQ ID NO: 2755)
I030F02	1223	141 - 252	164 - 176	192 - 198	231 - 241	1 - 125	26 - 37	52 - 67	100 - 114	AGYDILTGYPFYFDS (SEQ ID NO: 2757)
I030F05	1224	140 - 251	163 - 175	191 - 197	230 - 240	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I030F06	1225	139 - 251	162 - 175	191 - 197	230 - 240	1 - 123	26 - 35	50 - 66	99 - 112	RYGDPFYYYMMNV (SEQ ID NO: 2755)
I030F08	1226	140 - 254	163 - 176	192 - 198	231 - 243	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I030F09	1227	140 - 253	164 - 176	192 - 198	231 - 242	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I030F11	1228	139 - 250	162 - 174	190 - 196	229 - 239	1 - 123	26 - 35	50 - 66	99 - 112	RYGDPFYYYMMNV (SEQ ID NO: 2755)
I030F12	1229	140 - 251	163 - 175	191 - 197	230 - 240	1 - 124	26 - 35	50 - 66	99 - 113	DNYDILTGYSRFPD (SEQ ID NO: 2942)
I030G03	1230	140 - 256	163 - 176	192 - 202	237 - 245	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I030G07	1231	139 - 251	162 - 175	191 - 197	230 - 240	1 - 123	26 - 35	50 - 66	99 - 112	RYGDPFYYYMMNV (SEQ ID NO: 2755)
I030G09	1232	140 - 251	164 - 174	190 - 196	229 - 240	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I030H05	1233	145 - 255	168 - 181	197 - 203	236 - 244	1 - 129	26 - 35	50 - 66	99 - 118	DRGGNYDILTGYYFHHGVDV (SEQ ID NO: 2914)
I030H06	1234	146 - 258	170 - 182	198 - 204	239 - 247	1 - 130	26 - 37	52 - 69	102 - 119	ATKSYDILTRMYYYHMDV (SEQ ID NO: 2748)
I030H10	1235	140 - 253	163 - 176	192 - 198	231 - 242	1 - 124	26 - 35	50 - 66	99 - 113	DNYDILTGYSRFPD (SEQ ID NO: 2942)
I030H11	1236	140 - 252	164 - 176	192 - 198	231 - 241	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I031A01	1237	137 - 248	160 - 173	189 - 195	228 - 237	1 - 121	26 - 35	50 - 66	99 - 110	GYDSSAFRAFDI (SEQ ID NO: 2136)
I031A03	1238	141 - 251	166 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	PYYDPLTAYTFQYFGN (SEQ ID NO: 2806)
I031A08	1239	147 - 258	170 - 182	198 - 204	237 - 247	1 - 131	26 - 35	50 - 66	99 - 120	GREDTDKVKPWPDRYYHYHMDV (SEQ ID NO: 2809)
I031A12	1240	146 - 257	169 - 181	197 - 203	236 - 246	1 - 130	26 - 35	50 - 66	99 - 119	GREDTDKVKPWPDRYYHYHMDV (SEQ ID NO: 2972)
I031B03	1241	136 - 246	159 - 172	188 - 194	227 - 235	1 - 120	26 - 35	50 - 68	101 - 109	GLGHTDS (SEQ ID NO: 2959)
I031B06	1242	142 - 253	165 - 177	193 - 199	232 - 242	1 - 126	26 - 35	50 - 66	99 - 115	AKGYDSSGASDVFDV (SEQ ID NO: 2871)
I031B07	1243	147 - 258	170 - 182	198 - 204	237 - 247	1 - 131	26 - 35	50 - 66	99 - 120	GREDTDKVKPWPDRYYHYHMDV (SEQ ID NO: 2809)
I031B08	1244	147 - 260	171 - 183	199 - 205	238 - 249	1 - 131	26 - 35	50 - 66	99 - 120	SSPPKWDALTGHSYHSAMDV (SEQ ID NO: 2159)
I031B09	1245	147 - 258	170 - 182	198 - 204	237 - 247	1 - 131	26 - 35	50 - 66	99 - 120	SNPPKWDALTGHSYHSAMDV (SEQ ID NO: 2840)
I031B11	1246	137 - 248	160 - 172	188 - 194	227 - 237	1 - 121	26 - 35	50 - 66	99 - 110	GYDSSAFRAFDI (SEQ ID NO: 2136)
I031B12	1247	147 - 259	170 - 183	199 - 205	238 - 248	1 - 131	26 - 35	50 - 66	99 - 120	GREDTDKVKPWPDRYYHYHMDV (SEQ ID NO: 2809)
I031C01	1248	137 - 248	160 - 172	188 - 194	227 - 237	1 - 121	26 - 35	50 - 66	99 - 110	GYDSSAFRAFDI (SEQ ID NO: 2136)
I031C02	1249	141 - 253	164 - 177	193 - 199	232 - 242	1 - 125	26 - 35	50 - 66	99 - 114	PFYDTLTSYVFQYFDH (SEQ ID NO: 2137)
I031C04	1250	147 - 260	171 - 183	199 - 205	238 - 249	1 - 131	26 - 35	50 - 66	99 - 120	GRKDTKVKPWPDRYYHYHMDV (SEQ ID NO: 2813)
I031C08	1251	137 - 248	161 - 171	187 - 193	226 - 237	1 - 121	26 - 35	50 - 66	99 - 110	GYDSSAFRAFDI (SEQ ID NO: 2136)
I031C11	1252	147 - 257	171 - 181	197 - 203	236 - 246	1 - 131	26 - 35	50 - 66	99 - 120	GREDTDKVKPWPDRYYHYHMDV (SEQ ID NO: 2809)
I031D01	1253	145 - 256	168 - 180	196 - 202	235 - 245	1 - 129	26 - 35	50 - 66	99 - 118	AATTSQKHKNKYAYFYGMDV (SEQ ID NO: 2131)

35

40

45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Pro Phe Tyr Asp Thr Leu Thr Ser Tyr Val Trp Pro Ser Phe
100 105 110

Phe Ser Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr
130 135 140

Thr Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Glu Arg
145 150 155 160

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val
165 170 175

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr
180 185 190

Gly Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

Glu Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
210 215 220

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr
225 230 235 240

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
245 250

<210> 62

<211> 250

<212> PRT

<213> Homo sapiens

<400> 62

Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Pro Phe Tyr Asp Thr Leu Thr Ser Tyr Val Thr Pro Arg Gly
100 105 110

Tyr Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr Thr
130 135 140

Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
145 150 155 160

Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val Ala
165 170 175

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr Gly
180 185 190

Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser Glu
195 200 205

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp
210 215 220

Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr Phe

225 230 235 240

Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
245 250

<210> 63
<211> 250
<212> PRT
<213> Homo sapiens

<400> 63
Gln Val Gln Leu Val Gln Ser Val Val Glu Val Arg Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Pro Phe Tyr Asp Thr Leu Thr Ser Tyr Val Ser Ser Leu Leu
100 105 110

Ser Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr Thr
130 135 140

Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
145 150 155 160

Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val Ala
165 170 175

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr Gly
180 185 190

Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser Glu
195 200 205

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp
210 215 220

Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr Phe
225 230 235 240

Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
245 250

<210> 64
<211> 251
<212> PRT
<213> Homo sapiens

<400> 64
Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Pro Phe Tyr Asp Thr Leu Thr Ser Tyr Val Pro Leu Leu Pro
100 105 110

Leu Cys Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr
130 135 140

Thr Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Glu Arg
 145 150 155 160

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val
 165 170 175

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr
 180 185 190

Gly Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser
 195 200 205

Glu Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
 210 215 220

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr
 225 230 235 240

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
 245 250

<210> 65
 <211> 251
 <212> PRT
 <213> Homo sapiens

<400> 65
 Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His
 20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
 35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Pro Phe Tyr Asp Thr Leu Thr Ser Tyr Val Pro Pro Pro Ser
100 105 110

Phe Leu Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr
130 135 140

Thr Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Glu Arg
145 150 155 160

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val
165 170 175

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr
180 185 190

Gly Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

Glu Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
210 215 220

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr
225 230 235 240

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
245 250

<210> 66

<211> 250

<212> PRT

<213> Homo sapiens

<400> 66

Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe

50

55

60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Pro Phe Tyr Asp Thr Leu Thr Ser Tyr Val Pro Thr Ser Thr
100 105 110

Thr Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr Thr
130 135 140

Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
145 150 155 160

Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val Thr
165 170 175

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr Gly
180 185 190

Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser Glu
195 200 205

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp
210 215 220

Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr Phe
225 230 235 240

Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
245 250

<210> 67

<211> 251

<212> PRT

<213> Homo sapiens

<400> 67

Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Glu Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
 210 215 220

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr
 225 230 235 240

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
 245 250

<210> 69
 <211> 250
 <212> PRT
 <213> Homo sapiens

<400> 69
 Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His
 20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
 35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Pro Phe Tyr Asp Thr Leu Thr Ser Tyr Val Cys Arg His Leu
 100 105 110

Phe Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly
 115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr Thr
 130 135 140

Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
 145 150 155 160

Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val Ala
165 170 175

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr Gly
180 185 190

Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser Glu
195 200 205

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp
210 215 220

Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr Phe
225 230 235 240

Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
245 250

<210> 70
<211> 251
<212> PRT
<213> Homo sapiens

<400> 70
Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asp His
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Pro Phe Tyr Asp Thr Leu Thr Ser Tyr Val Val Ser Phe Pro
100 105 110

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
 35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Pro Phe Tyr Asp Thr Leu Thr Ser Tyr Val Leu Phe Arg Pro
 100 105 110

Val Leu Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr
 130 135 140

Thr Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Glu Arg
 145 150 155 160

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val
 165 170 175

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr
 180 185 190

Gly Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser
 195 200 205

Glu Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
 210 215 220

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Ser Arg Thr
 225 230 235 240

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
 245 250

<210> 73

<211> 250
 <212> PRT
 <213> Homo sapiens

<400> 73
 Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His
 20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
 35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Pro Phe Tyr Asp Thr Leu Thr Ser Tyr Val Pro Ser Val Gly
 100 105 110

Gly Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly
 115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr Thr
 130 135 140

Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
 145 150 155 160

Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val Ala
 165 170 175

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr Gly
 180 185 190

Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser Glu
 195 200 205

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp
 210 215 220

Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr Phe
 225 230 235 240

Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
 245 250

<210> 74
 <211> 250
 <212> PRT
 <213> Homo sapiens

<400> 74
 Gln Val Gln Leu Val Gln Pro Gly Val Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His
 20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
 35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Pro Phe Tyr Asp Thr Leu Thr Ser Tyr Val Pro Pro Thr Arg
 100 105 110

His Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly
 115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr Thr
 130 135 140

Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
 145 150 155 160

Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val Ala
 165 170 175

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr Gly
 180 185 190

Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser Glu
 195 200 205

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp
 210 215 220

Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr Phe
 225 230 235 240

Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
 245 250

<210> 75
 <211> 250
 <212> PRT
 <213> Homo sapiens

<400> 75
 Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His
 20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
 35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Pro Phe Tyr Asp Thr Leu Thr Ser Tyr Val Leu Arg Ser Arg
 100 105 110

Asp Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly
 115 120 125

85

90

95

Ala Arg Pro Phe Tyr Asp Thr Leu Thr Ser Tyr Val Pro Leu Leu Pro
 100 105 110

Pro Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly
 115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr Thr
 130 135 140

Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
 145 150 155 160

Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val Ala
 165 170 175

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr Gly
 180 185 190

Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser Glu
 195 200 205

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp
 210 215 220

Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr Phe
 225 230 235 240

Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
 245 250

<210> 77

<211> 250

<212> PRT

<213> Homo sapiens

<400> 77

Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His
 20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
 35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Pro Phe Tyr Asp Thr Leu Thr Ser Tyr Val Leu Arg Cys Val
 100 105 110

Leu Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly
 115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr Thr
 130 135 140

Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
 145 150 155 160

Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val Ala
 165 170 175

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr Gly
 180 185 190

Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser Glu
 195 200 205

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp
 210 215 220

Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr Phe
 225 230 235 240

Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
 245 250

<210> 78

<211> 250

<212> PRT

<213> Homo sapiens

I033C08	1290	142 - 249	163 - 173	189 - 195	228 - 238	1 - 126	26 - 35	50 - 66	99 - 115	EMGYDILTGYYLNYMDV (SEQ ID NO: 2862)
I033D02	1291	138 - 245	161 - 171	187 - 193	226 - 234	1 - 122	26 - 35	50 - 66	99 - 111	GDYDILTGYYMDV (SEQ ID NO: 2781)
I033D03	1292	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDFDI (SEQ ID NO: 2153)
I033D05	1293	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDFDI (SEQ ID NO: 2153)
I033D11	1294	140 - 247	161 - 171	187 - 193	226 - 236	1 - 124	26 - 35	50 - 66	99 - 113	VKRDILTGYYVEGMDV (SEQ ID NO: 2869)
I033D12	1295	144 - 254	166 - 179	195 - 201	234 - 243	1 - 128	26 - 35	50 - 66	99 - 117	GGPHYDILTGYYMAVGFDI (SEQ ID NO: 2962)
I033E01	1296	139 - 249	161 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	DIDARLAALDAFDI (SEQ ID NO: 2794)
I033E06	1297	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATHDPLTGYSFDFDI (SEQ ID NO: 2780)
I033E11	1298	143 - 253	165 - 177	193 - 199	232 - 242	1 - 127	26 - 35	50 - 66	99 - 116	HRSCSTSCRNDAFDI (SEQ ID NO: 2770)
I033E12	1299	142 - 249	163 - 173	189 - 195	228 - 238	1 - 126	26 - 35	50 - 66	99 - 115	EMGYDILTGYYLNYMDV (SEQ ID NO: 2862)
I033F03	1300	139 - 246	160 - 170	186 - 192	225 - 235	1 - 123	26 - 35	50 - 66	99 - 112	EGAADYLNQYFQD (SEQ ID NO: 2768)
I033F08	1301	145 - 256	167 - 179	195 - 201	234 - 245	1 - 129	26 - 35	50 - 66	99 - 118	QKVYYDILTGYYYYGMDV (SEQ ID NO: 2767)
I033F10	1302	144 - 254	166 - 179	195 - 201	234 - 243	1 - 128	26 - 35	50 - 66	99 - 117	EVRYDILTRSYLAGPLDN (SEQ ID NO: 2751)
I033F12	1303	134 - 241	155 - 165	181 - 187	220 - 230	1 - 118	26 - 35	50 - 66	99 - 107	DIDIGDDDS (SEQ ID NO: 2954)
I033G01	1304	143 - 253	165 - 178	194 - 200	233 - 242	1 - 127	24 - 33	48 - 64	97 - 116	EGGNYDILTGYYIGNGAFDI (SEQ ID NO: 2158)
I033G03	1305	142 - 249	163 - 173	189 - 195	228 - 238	1 - 126	26 - 35	50 - 66	99 - 115	PQGVTLVRGAETDAFAI (SEQ ID NO: 2925)
I033G08	1306	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDFDI (SEQ ID NO: 2153)
I033H04	1307	140 - 247	161 - 171	187 - 193	226 - 236	1 - 124	25 - 34	49 - 65	98 - 113	ATYDPLTGYSFDFDI (SEQ ID NO: 2153)
I037A05	1308	139 - 246	160 - 170	186 - 192	225 - 235	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLFPHYGMDV (SEQ ID NO: 2133)
I037B03	1309	141 - 251	163 - 175	191 - 197	230 - 240	1 - 125	26 - 35	50 - 66	99 - 114	SHYDILTRLNYWYFDL (SEQ ID NO: 2950)
I037B04	1310	144 - 251	167 - 177	193 - 199	232 - 241	1 - 128	26 - 35	50 - 66	99 - 117	DPGYDILTGYYHRYGMDV (SEQ ID NO: 2922)
I037C04	1311	142 - 252	164 - 177	193 - 199	232 - 241	1 - 126	26 - 35	50 - 65	98 - 115	ENGDYDILTGQTFYGMVDV (SEQ ID NO: 2752)
I037C06	1312	141 - 249	163 - 173	189 - 195	228 - 238	1 - 125	26 - 35	50 - 66	99 - 114	LYYDILTGYYHWDADF (SEQ ID NO: 2882)
I037C08	1313	140 - 250	162 - 175	191 - 197	230 - 239	1 - 124	26 - 35	50 - 66	99 - 113	DGIDILLVPAALMDV (SEQ ID NO: 2160)
I037D11	1314	136 - 246	158 - 171	187 - 193	226 - 235	1 - 120	26 - 35	50 - 66	99 - 109	SQWLEHVDVFI (SEQ ID NO: 2864)
I037E06	1315	144 - 251	165 - 175	191 - 197	230 - 240	1 - 128	26 - 35	50 - 66	99 - 117	DRRDYDILTRYYYGMDV (SEQ ID NO: 2928)
I037F04	1316	144 - 251	165 - 175	191 - 197	230 - 240	1 - 128	26 - 35	50 - 65	98 - 117	KQRGDYDILTGYYLGYAFDI (SEQ ID NO: 2808)
I037G01	1317	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	SHYDILTRLNYWYFDL (SEQ ID NO: 2950)
I037G03	1318	146 - 256	168 - 181	197 - 203	236 - 245	1 - 130	26 - 35	50 - 66	99 - 119	DLGSFYDILTALRENYGMDV (SEQ ID NO: 2963)
I037G10	1319	140 - 250	162 - 175	191 - 197	230 - 239	1 - 124	26 - 35	50 - 66	99 - 113	DYYDILTKLPYGMDV (SEQ ID NO: 2975)
I042A07	1320	144 - 251	167 - 177	193 - 199	232 - 240	1 - 128	26 - 35	50 - 66	99 - 117	VSPSYDILTGYYLPHAFDV (SEQ ID NO: 2849)
I042A10	1321	142 - 249	165 - 175	191 - 197	230 - 238	1 - 126	26 - 35	50 - 65	98 - 115	GPRYYDILTGYYRWNWFD (SEQ ID NO: 2801)
I042B03	1322	140 - 247	161 - 171	187 - 193	226 - 236	1 - 124	26 - 35	50 - 66	99 - 113	DIDDLTGYYVLGMDV (SEQ ID NO: 2924)
I042B12	1323	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	SHYDILTGLNYWYFDL (SEQ ID NO: 2166)
I042D01	1324	136 - 246	158 - 171	187 - 193	226 - 235	1 - 120	26 - 35	50 - 66	99 - 109	QQWLPHYDAFDI (SEQ ID NO: 2839)
I042D03	1325	140 - 250	162 - 175	191 - 197	230 - 239	1 - 124	26 - 35	50 - 68	101 - 113	AYYDILTGYYFDI (SEQ ID NO: 2873)

I042D10	1326	142 - 252	164 - 177	193 - 199	232 - 241	1 - 126	26 - 35	50 - 65	98 - 115	ERADYDILTGYYFYGMVDV (SEQ ID NO: 2802)
I042E10	1327	147 - 257	169 - 182	198 - 204	237 - 246	1 - 131	26 - 37	52 - 69	102 - 120	ERPYYDILTGYYTVTYGMVDV (SEQ ID NO: 2798)
I042E11	1328	140 - 247	161 - 171	187 - 193	226 - 236	1 - 124	26 - 35	50 - 66	99 - 113	DEYDILTGLLQGMVDV (SEQ ID NO: 2883)
I042F08	1329	142 - 252	164 - 177	193 - 199	232 - 241	1 - 126	26 - 37	52 - 67	100 - 115	GDYDILTGYPPLHAFDI (SEQ ID NO: 2738)
I042F12	1330	140 - 247	161 - 171	187 - 193	226 - 236	1 - 124	26 - 35	50 - 66	99 - 113	DGYDILTGYYFGMDV (SEQ ID NO: 2976)
I042G08	1331	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	EHYDILTGYSLLGMDV (SEQ ID NO: 2907)
I042G10	1332	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	SHYDILTGLNYYWYFDL (SEQ ID NO: 2166)
I042H03	1333	143 - 253	165 - 178	194 - 200	233 - 242	1 - 127	26 - 35	50 - 65	98 - 116	GSLYDILTGYYIGNAFDI (SEQ ID NO: 2759)
I043A03	1334	144 - 254	166 - 179	195 - 201	234 - 243	1 - 128	26 - 35	50 - 66	99 - 117	DGYYDILTGFFYYFGMDV (SEQ ID NO: 2899)
I043B02	1335	142 - 249	163 - 173	189 - 195	228 - 238	1 - 126	26 - 35	50 - 65	98 - 115	GGYYDILTGVLVYYGMVDV (SEQ ID NO: 2744)
I043B03	1336	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I043B06	1337	143 - 253	165 - 178	194 - 200	233 - 242	1 - 127	26 - 35	50 - 66	99 - 116	DQYDILTGHHIDYYMDV (SEQ ID NO: 2828)
I043B07	1338	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I043B09	1339	143 - 253	165 - 178	194 - 200	233 - 242	1 - 127	26 - 35	50 - 65	98 - 116	HVRDYDILTGYYRGHHFDY (SEQ ID NO: 2727)
I043D11	1340	144 - 254	166 - 179	195 - 201	234 - 243	1 - 128	26 - 35	50 - 66	99 - 117	EVKNYDILTRSYLAGPLDN (SEQ ID NO: 2751)
I043E05	1341	143 - 250	164 - 174	190 - 196	229 - 239	1 - 127	26 - 35	50 - 66	99 - 116	TESNYDILTGYYWPSMDV (SEQ ID NO: 2940)
I043F01	1342	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I043F04	1343	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I043F12	1344	143 - 250	164 - 174	190 - 196	229 - 239	1 - 127	26 - 35	50 - 66	99 - 116	TESNYDILTGYYWPSMDV (SEQ ID NO: 2940)
I043H07	1345	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I044A11	1346	144 - 251	165 - 175	191 - 197	230 - 240	1 - 128	26 - 35	50 - 68	101 - 117	APYDILTGYSDDYYGMVDV (SEQ ID NO: 2968)
I044B11	1347	139 - 249	161 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	DSDARLAALDAFDI (SEQ ID NO: 2978)
I044C09	1348	140 - 250	162 - 174	190 - 196	229 - 239	1 - 124	26 - 35	50 - 66	99 - 113	GQFGVLPNYYHMDV (SEQ ID NO: 2943)
I044C10	1349	143 - 253	165 - 177	193 - 199	232 - 242	1 - 127	26 - 35	50 - 66	99 - 116	DIKRYNSNWPYYDYMDV (SEQ ID NO: 2726)
I044D03	1350	144 - 254	166 - 179	195 - 201	234 - 243	1 - 128	26 - 35	50 - 66	99 - 117	DKQYYDILTGDPVEGGMDV (SEQ ID NO: 2889)
I044D09	1351	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I044E07	1352	137 - 247	159 - 172	188 - 194	227 - 236	1 - 121	26 - 35	50 - 66	99 - 110	AGSSLVTYGTDV (SEQ ID NO: 2825)
I044E11	1353	143 - 253	165 - 178	194 - 200	233 - 242	1 - 127	26 - 35	50 - 66	99 - 116	SDDYDILTGNVVGSLDY (SEQ ID NO: 2758)
I044F07	1354	147 - 257	169 - 182	198 - 204	237 - 246	1 - 131	26 - 35	50 - 66	99 - 120	DGRLSYDILTGYYARDYYGMVDV (SEQ ID NO: 2912)
I044G02	1355	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I044G07	1356	149 - 259	171 - 184	200 - 206	239 - 248	1 - 133	26 - 35	50 - 66	99 - 122	DQNHPIYDILTGYYVPTGPLLKN (SEQ ID NO: 2845)
I044H01	1357	144 - 251	165 - 175	191 - 197	230 - 240	1 - 128	26 - 35	50 - 66	99 - 117	EVKNYDILTRSYLAGPLDN (SEQ ID NO: 2751)
I050A01	1358	141 - 253	164 - 177	193 - 199	232 - 242	1 - 125	26 - 35	50 - 66	99 - 114	DMGYDILTGYYGAFDI (SEQ ID NO: 2946)
I050B12	1359	141 - 253	164 - 177	193 - 199	232 - 242	1 - 125	26 - 35	50 - 66	99 - 114	DYDVLTFGLDGMVDV (SEQ ID NO: 2829)
I050C06	1360	140 - 248	165 - 175	191 - 197	230 - 237	1 - 124	26 - 35	50 - 65	98 - 113	DHYDVLTGSLYLAQFDV (SEQ ID NO: 2728)
I050C08	1361	141 - 253	164 - 177	193 - 199	232 - 242	1 - 125	26 - 37	52 - 67	100 - 114	GRYDFTGYYLRNFDY (SEQ ID NO: 2731)

I050E01	1362	140 - 252	163 - 176	192 - 198	231 - 241	1 - 124	26 - 35	50 - 66	99 - 113	GHYDILTGYVFGFDY (SEQ ID NO: 2886)
I050E10	1363	137 - 248	160 - 172	188 - 194	227 - 237	1 - 121	26 - 35	50 - 66	99 - 110	DMKVVYKYALDV (SEQ ID NO: 2823)
I050H08	1364	141 - 253	164 - 177	193 - 199	232 - 242	1 - 125	26 - 35	50 - 66	99 - 114	DLRYDILTGYHDAFDI (SEQ ID NO: 2890)
I051A04	1365	147 - 258	170 - 183	199 - 205	238 - 247	1 - 131	26 - 35	50 - 66	99 - 120	SSPPKWYDALTGSSYHSAMDV (SEQ ID NO: 2159)
I051A08	1366	141 - 252	164 - 176	192 - 198	231 - 241	1 - 125	26 - 35	50 - 66	99 - 114	HRRARVVVPVGAMDV (SEQ ID NO: 2930)
I051A12	1367	143 - 250	164 - 174	190 - 196	229 - 239	1 - 127	26 - 35	50 - 66	99 - 116	DGSYDILTGYIDNYMDV (SEQ ID NO: 2930)
I051B08	1368	142 - 253	165 - 177	193 - 199	232 - 242	1 - 126	26 - 36	51 - 67	100 - 115	RSMMVTTAPYDAFDL (SEQ ID NO: 2154)
I051C06	1369	135 - 246	158 - 170	186 - 192	225 - 235	1 - 119	26 - 35	50 - 66	99 - 108	DTVRSAGMDV (SEQ ID NO: 2785)
I051G12	1370	143 - 250	164 - 174	190 - 196	229 - 239	1 - 127	26 - 35	50 - 66	99 - 116	DGSYDILTGYIDNYMDV (SEQ ID NO: 2804)
I055A05	1371	133 - 244	156 - 169	185 - 191	224 - 233	1 - 117	26 - 35	50 - 66	99 - 106	SGPGWFDP (SEQ ID NO: 2154)
I055A11	1372	133 - 244	156 - 169	185 - 191	224 - 233	1 - 117	26 - 35	50 - 66	99 - 106	SGPGWFDP (SEQ ID NO: 2870)
I061A03	1373	140 - 251	163 - 176	192 - 198	231 - 240	1 - 124	26 - 34	49 - 65	98 - 113	ELGSSIVGATTGALDM (SEQ ID NO: 2852)
I061A04	1374	141 - 251	165 - 175	191 - 197	230 - 240	1 - 125	26 - 35	50 - 66	99 - 114	GDYDILTGYPAECFQI (SEQ ID NO: 2854)
I061A08	1375	140 - 253	164 - 176	192 - 198	233 - 242	1 - 124	26 - 35	50 - 66	99 - 113	DNVDILTGYSRFP (SEQ ID NO: 2942)
I061A09	1376	140 - 252	164 - 176	192 - 198	231 - 241	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I061A10	1377	140 - 249	163 - 173	189 - 195	228 - 238	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I061B07	1378	140 - 252	163 - 176	192 - 198	231 - 241	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I061B09	1379	143 - 253	165 - 178	194 - 200	233 - 242	1 - 127	24 - 33	48 - 64	97 - 116	EGGNYDILTGYIYNGAFDI (SEQ ID NO: 2158)
I061B12	1380	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDFDI (SEQ ID NO: 2153)
I061C12	1381	138 - 248	160 - 173	189 - 195	228 - 237	1 - 122	26 - 35	50 - 66	99 - 111	TYVDILTGYHFDY (SEQ ID NO: 2788)
I061D01	1382	137 - 247	159 - 172	188 - 194	227 - 236	1 - 121	26 - 35	50 - 68	101 - 110	GPVGIGNYDY (SEQ ID NO: 2749)
I061D03	1383	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDFDI (SEQ ID NO: 2153)
I061D04	1384	140 - 247	161 - 171	187 - 193	226 - 236	1 - 124	26 - 35	50 - 66	99 - 113	AVLRYAGLQGAFFI (SEQ ID NO: 2970)
I061D07	1385	141 - 248	164 - 174	190 - 196	229 - 237	1 - 125	26 - 35	50 - 66	99 - 114	VSGYNSGYFESYDMDV (SEQ ID NO: 2732)
I061D09	1386	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	LNLEKTVVRGFGYFDL (SEQ ID NO: 2952)
I061D10	1387	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	DHYDILTGLYYYGMDV (SEQ ID NO: 2760)
I061E01	1388	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	LNLEKTVVRGFGYFDL (SEQ ID NO: 2952)
I061E05	1389	142 - 251	163 - 175	191 - 197	230 - 240	1 - 126	26 - 35	50 - 66	99 - 115	GGELVWFGESDYGMDV (SEQ ID NO: 2787)
I061E09	1390	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDFDI (SEQ ID NO: 2153)
I061E12	1391	133 - 240	154 - 164	180 - 186	219 - 229	1 - 117	26 - 35	50 - 66	99 - 106	SQRLFIDS (SEQ ID NO: 2842)
I061F01	1392	146 - 256	168 - 181	197 - 203	236 - 245	1 - 130	26 - 35	50 - 66	99 - 119	DRYVDILTGYIPGLDDAFDI (SEQ ID NO: 2887)
I061F09	1393	139 - 246	160 - 170	186 - 192	225 - 235	1 - 123	26 - 35	50 - 66	99 - 112	DSDARLAALDAFFI (SEQ ID NO: 2978)
I061F10	1394	145 - 252	166 - 176	192 - 198	231 - 241	1 - 129	26 - 35	50 - 66	99 - 118	EESYDILTGYVHYGMDV (SEQ ID NO: 2743)
I061F11	1395	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYFDGFDI (SEQ ID NO: 2949)
I061G01	1396	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDFDI (SEQ ID NO: 2153)
I061G03	1397	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	AYYDILTGLFLPYMDL (SEQ ID NO: 2771)

I061G09	1398	144 - 254	166 - 179	195 - 201	234 - 243	1 - 128	26 - 35	50 - 66	99 - 117	EVRYDILTRSYLAGPLDN (SEQ ID NO: 2751)
I061G10	1399	143 - 253	165 - 178	194 - 200	233 - 242	1 - 127	26 - 35	50 - 65	98 - 116	EGSYDILTGYYVGVGRMDV (SEQ ID NO: 2171)
I061G11	1400	137 - 247	159 - 171	187 - 193	226 - 236	1 - 121	26 - 35	50 - 68	101 - 110	RDILTGFDYS (SEQ ID NO: 2933)
I061H05	1401	142 - 252	164 - 177	193 - 199	232 - 241	1 - 126	26 - 37	52 - 67	100 - 115	ATYDPLTGYSFSGFDI (SEQ ID NO: 2153)
I064A05	1402	142 - 249	163 - 173	189 - 195	228 - 238	1 - 126	26 - 35	50 - 68	101 - 115	DFYDILTGYYHQHGMV (SEQ ID NO: 2919)
I064A11	1403	138 - 248	160 - 173	189 - 195	228 - 237	1 - 122	26 - 35	50 - 66	99 - 111	HSKEYNWNYYALDY (SEQ ID NO: 2754)
I064B01	1404	138 - 248	160 - 173	189 - 195	228 - 237	1 - 122	26 - 35	50 - 66	99 - 111	TRMDVLTRYSDY (SEQ ID NO: 2750)
I064B02	1405	144 - 254	166 - 179	195 - 201	234 - 243	1 - 128	26 - 35	50 - 66	99 - 117	AFEDYDILTGYYHHDAFDI (SEQ ID NO: 2911)
I064B12	1406	133 - 243	155 - 168	184 - 190	223 - 232	1 - 117	26 - 35	50 - 66	99 - 106	PSYHYMDV (SEQ ID NO: 2740)
I064C06	1407	145 - 255	167 - 180	196 - 202	235 - 244	1 - 129	26 - 35	50 - 66	99 - 118	VNADYDILTGYPDDYYGMDV (SEQ ID NO: 2819)
I064D01	1408	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFSGFDI (SEQ ID NO: 2153)
I064D02	1409	146 - 256	168 - 181	197 - 203	236 - 245	1 - 130	26 - 35	50 - 66	99 - 119	EDATYDILTGYYMGSGMDV (SEQ ID NO: 2763)
I064E01	1410	143 - 250	166 - 176	192 - 198	231 - 239	1 - 127	26 - 35	50 - 66	99 - 116	ETRKYTSSPPYNYVYMDV (SEQ ID NO: 2736)
I064E02	1411	140 - 251	162 - 174	190 - 196	229 - 240	1 - 124	26 - 35	50 - 66	99 - 113	RDYDILTGYSRGFDP (SEQ ID NO: 2725)
I064E03	1412	144 - 254	166 - 179	195 - 201	234 - 243	1 - 128	26 - 35	50 - 65	99 - 117	DGIYDILTLVSYNGMDV (SEQ ID NO: 2775)
I064E07	1413	140 - 250	162 - 175	191 - 197	230 - 239	1 - 124	26 - 35	50 - 65	98 - 113	GERDILTGYYLDGMDV (SEQ ID NO: 2948)
I064E08	1414	140 - 250	162 - 174	190 - 196	229 - 239	1 - 124	26 - 35	50 - 66	99 - 113	ERGSYSSGYSYGAFDV (SEQ ID NO: 2898)
I064F05	1415	142 - 252	164 - 177	193 - 199	232 - 241	1 - 126	26 - 35	50 - 66	99 - 115	ESGGYSYGSRDYYGMDV (SEQ ID NO: 2836)
I064F08	1416	145 - 252	166 - 176	192 - 198	231 - 241	1 - 129	26 - 35	50 - 66	99 - 118	DRGVGYDILTGRTYYGMDV (SEQ ID NO: 2900)
I064G06	1417	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFSGFDI (SEQ ID NO: 2153)
I065A12	1418	143 - 253	165 - 178	194 - 200	233 - 242	1 - 127	26 - 35	50 - 66	99 - 116	DVSGHDILTGYSRYFDV (SEQ ID NO: 2795)
I065C04	1419	139 - 249	161 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	GQKNYYESSGYLEH (SEQ ID NO: 2916)
I065C09	1420	140 - 250	162 - 174	190 - 196	229 - 239	1 - 124	26 - 35	50 - 66	99 - 113	GDYDILTGYSYSHFDY (SEQ ID NO: 2908)
I065E02	1421	141 - 248	164 - 174	190 - 196	229 - 237	1 - 125	26 - 35	50 - 66	99 - 114	AYDYDILTGYSYFYDY (SEQ ID NO: 2895)
I065E04	1422	135 - 245	157 - 169	185 - 191	224 - 234	1 - 119	26 - 35	50 - 66	99 - 108	GMGDHYGMDV (SEQ ID NO: 2161)
I065F03	1423	137 - 247	159 - 172	188 - 194	227 - 236	1 - 121	26 - 35	50 - 66	99 - 110	AGSSLMYGTDV (SEQ ID NO: 2773)
I065G06	1424	135 - 242	156 - 166	182 - 188	221 - 231	1 - 119	26 - 35	50 - 66	99 - 108	GMGDHYGMDV (SEQ ID NO: 2161)
I065G07	1425	142 - 249	163 - 173	189 - 195	228 - 238	1 - 126	26 - 35	50 - 66	99 - 115	GGNYDILTGYYIGAFDI (SEQ ID NO: 2824)
I065G08	1426	139 - 246	160 - 170	186 - 192	225 - 235	1 - 123	26 - 35	50 - 66	99 - 112	SRDILLPHYGMDV (SEQ ID NO: 2133)
I065H06	1427	144 - 254	166 - 179	195 - 201	234 - 243	1 - 128	26 - 35	50 - 66	99 - 117	GYEYDILTGYNELGAFDI (SEQ ID NO: 2851)
I066A03	1428	144 - 254	166 - 179	195 - 201	234 - 243	1 - 128	26 - 35	50 - 66	99 - 117	DGTYYDILTGYYNQYGMV (SEQ ID NO: 2915)
I066A08	1429	137 - 247	159 - 171	187 - 193	226 - 236	1 - 121	26 - 35	50 - 66	99 - 110	AGSSLMYGTDV (SEQ ID NO: 2773)
I066A09	1430	135 - 245	157 - 169	185 - 191	224 - 234	1 - 119	26 - 35	50 - 66	99 - 108	GMGDHYGMDV (SEQ ID NO: 2161)
I066A10	1431	142 - 252	164 - 177	193 - 199	232 - 241	1 - 126	26 - 35	50 - 66	99 - 115	DRGYDILTGYYYYGMDV (SEQ ID NO: 2876)
I066A11	1432	143 - 253	165 - 178	194 - 200	233 - 242	1 - 127	26 - 35	50 - 66	99 - 116	EVRYDILTGYYISYMDV (SEQ ID NO: 2778)
I066B02	1433	135 - 242	156 - 166	182 - 188	221 - 231	1 - 119	26 - 35	50 - 66	99 - 108	GMGDHYGMDV (SEQ ID NO: 2161)

I066B08	1434	137 - 247	159 - 172	188 - 194	227 - 236	1 - 121	26 - 35	50 - 66	99 - 110	AGSSLMYGTDV (SEQ ID NO: 2773)
I066B10	1435	142 - 252	164 - 177	193 - 199	232 - 241	1 - 126	26 - 35	50 - 66	99 - 115	GLYFEDTNYRHGDAFDI (SEQ ID NO: 2790)
I066C02	1436	135 - 245	157 - 169	185 - 191	224 - 234	1 - 119	26 - 35	50 - 66	99 - 108	GMGDHYGMDV (SEQ ID NO: 2161)
I066C11	1437	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDFDI (SEQ ID NO: 2153)
I066C12	1438	135 - 242	156 - 166	182 - 188	221 - 231	1 - 119	26 - 35	50 - 66	99 - 108	GMGDHYGMDV (SEQ ID NO: 2161)
I066D06	1439	140 - 250	162 - 175	191 - 197	230 - 239	1 - 124	26 - 35	50 - 66	99 - 113	ENYDFLTGYGAFDI (SEQ ID NO: 2772)
I066D08	1440	138 - 248	160 - 173	189 - 195	228 - 237	1 - 122	26 - 35	50 - 66	99 - 111	HSKEYWNYYALDY (SEQ ID NO: 2754)
I066D11	1441	144 - 254	166 - 179	195 - 201	234 - 243	1 - 128	26 - 35	50 - 66	99 - 117	ERSQDFLTGVDRYHPMDV (SEQ ID NO: 2956)
I066D12	1442	139 - 249	161 - 174	190 - 196	229 - 238	1 - 123	26 - 35	50 - 66	99 - 112	EGAADYLNQYFQH (SEQ ID NO: 2815)
I066E06	1443	137 - 247	159 - 171	187 - 193	226 - 236	1 - 121	26 - 35	50 - 66	99 - 110	AGSSLMYGTDV (SEQ ID NO: 2773)
I066E12	1444	135 - 242	156 - 166	182 - 188	221 - 231	1 - 119	26 - 35	50 - 66	99 - 108	GMGDHYGMDV (SEQ ID NO: 2161)
I066G05	1445	142 - 249	163 - 173	189 - 195	228 - 238	1 - 126	26 - 35	50 - 66	99 - 115	GLYFEDTNYRHGDAFDI (SEQ ID NO: 2790)
I066G08	1446	141 - 248	164 - 174	190 - 196	229 - 237	1 - 125	26 - 35	50 - 66	99 - 114	VYYDILTGHPTYGMDV (SEQ ID NO: 2791)
I066G10	1447	144 - 254	166 - 178	194 - 200	233 - 243	1 - 128	26 - 35	50 - 68	101 - 117	GIYDILTGYHWDADFID (SEQ ID NO: 2872)
I066G12	1448	143 - 254	165 - 177	193 - 199	232 - 243	1 - 127	26 - 35	50 - 66	99 - 116	ESTYDILTGSYHDYGLDV (SEQ ID NO: 2822)
I066H04	1449	143 - 253	165 - 178	194 - 200	233 - 242	1 - 127	26 - 35	50 - 65	98 - 116	DRLHYDILTGHQTDADFID (SEQ ID NO: 2885)
I067A07	1450	144 - 254	166 - 179	195 - 201	234 - 243	1 - 128	26 - 35	50 - 66	99 - 117	VLTNYYDILTGYREDAFDM (SEQ ID NO: 2939)
I067A11	1451	135 - 245	157 - 170	186 - 192	225 - 234	1 - 119	26 - 35	50 - 66	99 - 108	GMGDHYGMDV (SEQ ID NO: 2161)
I067B08	1452	149 - 259	171 - 184	200 - 206	239 - 248	1 - 133	26 - 35	50 - 66	99 - 122	DRGASNYDILTGYYPAPAGVAFDI (SEQ ID NO: 2969)
I067C08	1453	148 - 258	170 - 183	199 - 205	238 - 247	1 - 132	26 - 37	52 - 69	102 - 121	EGAHYDILTGHNYHYGMDV (SEQ ID NO: 2747)
I067C09	1454	143 - 253	165 - 178	194 - 200	233 - 242	1 - 127	26 - 35	50 - 66	99 - 116	ETRKYTSSPPNYYYMDV (SEQ ID NO: 2736)
I067D07	1455	137 - 247	159 - 171	187 - 193	226 - 236	1 - 121	26 - 35	50 - 66	99 - 110	AGSSLMYGTDV (SEQ ID NO: 2773)
I067E01	1456	140 - 248	164 - 174	190 - 196	229 - 238	1 - 124	26 - 35	50 - 66	99 - 113	DQHDILTGVYYGMDV (SEQ ID NO: 2921)
I067E06	1457	135 - 245	157 - 169	185 - 191	224 - 234	1 - 119	26 - 35	50 - 66	99 - 108	GMGDHYGMDV (SEQ ID NO: 2161)
I067E07	1458	150 - 260	172 - 184	200 - 206	239 - 249	1 - 134	26 - 35	50 - 67	100 - 123	DYPGSEYDILTGYLFGYYGMDV (SEQ ID NO: 2926)
I067E11	1459	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDFDI (SEQ ID NO: 2153)
I067G03	1460	140 - 250	162 - 175	191 - 197	230 - 239	1 - 124	26 - 35	50 - 66	99 - 113	ARRVGVLGKNAFEI (SEQ ID NO: 2765)
I067G05	1461	140 - 250	162 - 174	190 - 196	229 - 239	1 - 124	26 - 35	50 - 66	99 - 113	DQHDILTGGYYGMDV (SEQ ID NO: 2894)
I067G12	1462	141 - 252	163 - 176	192 - 198	231 - 241	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDFDI (SEQ ID NO: 2153)
I067H05	1463	146 - 256	168 - 180	196 - 202	235 - 245	1 - 130	26 - 35	50 - 68	101 - 119	EGTYDILTGYPLGVFDY (SEQ ID NO: 2936)
I067H06	1464	135 - 245	157 - 169	185 - 191	224 - 234	1 - 119	26 - 35	50 - 66	99 - 108	GMGDHYGMDV (SEQ ID NO: 2161)
I068C09	1465	137 - 248	160 - 172	188 - 194	227 - 237	1 - 121	26 - 35	50 - 66	99 - 110	GGSSQNFYGMDV (SEQ ID NO: 2884)
I068G03	1466	143 - 254	166 - 178	194 - 200	233 - 243	1 - 127	26 - 35	50 - 66	99 - 116	GTGYDILTGYMGSAFDQ (SEQ ID NO: 2800)
I068G04	1467	142 - 252	165 - 178	194 - 200	233 - 241	1 - 126	26 - 35	50 - 66	99 - 115	GVVWVAYGDVGIYGFVD (SEQ ID NO: 2937)
I068G07	1468	140 - 251	164 - 174	190 - 196	229 - 240	1 - 124	26 - 35	50 - 66	99 - 113	HDYYIMTAAHYYYDS (SEQ ID NO: 2909)
I068G08	1469	143 - 254	166 - 178	194 - 200	233 - 243	1 - 127	26 - 35	50 - 66	99 - 116	GIGYDILLTGYFTGSPLDY (SEQ ID NO: 2846)

I070F07	1470	140 - 247	161 - 171	187 - 193	226 - 236	1 - 124	26 - 35	50 - 66	99 - 113	DFYDILTGYPHDAFDI (SEQ ID NO: 2910)
I070G05	1471	140 - 250	162 - 175	191 - 197	230 - 239	1 - 124	26 - 35	50 - 68	101 - 113	DVDDILTGYSWDY (SEQ ID NO: 2867)
I070H02	1472	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	MEYDILTGYYGGYFDY (SEQ ID NO: 2179)
I071A01	1473	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	AAAYDPLTGYSFDFDI (SEQ ID NO: 2783)
I071A03	1474	143 - 250	164 - 174	190 - 196	229 - 239	1 - 127	26 - 35	50 - 66	99 - 116	DMHYDILTGYYTGLAFDM (SEQ ID NO: 2917)
I071B08	1475	142 - 252	166 - 176	192 - 198	231 - 241	1 - 126	27 - 36	51 - 67	100 - 115	GGYDILTQYPAEFFHP (SEQ ID NO: 2764)
I071E01	1476	138 - 248	160 - 173	189 - 195	228 - 237	1 - 122	26 - 35	50 - 66	99 - 111	DFGVIGDYRPFY (SEQ ID NO: 2777)
I071F11	1477	135 - 245	157 - 169	185 - 191	224 - 234	1 - 119	26 - 35	50 - 66	99 - 108	SSNPVYGLDV (SEQ ID NO: 2957)
I071G11	1478	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDFDI (SEQ ID NO: 2153)
I071H08	1479	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDFDI (SEQ ID NO: 2153)
I074A02	1480	141 - 250	164 - 174	190 - 196	229 - 239	1 - 125	26 - 35	50 - 66	99 - 114	DDRDILTNYYLEYFQH (SEQ ID NO: 2868)
I074A08	1481	147 - 259	170 - 182	198 - 204	237 - 248	1 - 131	26 - 35	50 - 66	99 - 120	SSPKWYDALTGDSYHSAMDV (SEQ ID NO: 2165)
I074D10	1482	144 - 253	168 - 178	194 - 200	233 - 242	1 - 128	26 - 35	50 - 66	99 - 117	DKTLGDQLVEAYYYDGMVDV (SEQ ID NO: 2776)
I074E01	1483	144 - 255	168 - 178	194 - 200	233 - 244	1 - 128	26 - 35	50 - 66	99 - 117	LGRTSRDILTGYPHYNMVDV (SEQ ID NO: 2944)
I074E02	1484	140 - 250	164 - 174	190 - 196	229 - 239	1 - 124	26 - 35	50 - 66	99 - 113	DDYDILTGSLYYFDS (SEQ ID NO: 2803)
I074E08	1485	143 - 259	166 - 179	195 - 205	240 - 248	1 - 127	26 - 35	50 - 66	99 - 116	GTGYDILTGYYMGSAFDQ (SEQ ID NO: 2800)
I074F12	1486	140 - 250	164 - 174	190 - 196	229 - 239	1 - 124	26 - 35	50 - 66	99 - 113	DRADILTGYNDAFDI (SEQ ID NO: 2739)
I074H06	1487	139 - 251	162 - 175	191 - 197	230 - 240	1 - 123	26 - 35	50 - 66	99 - 112	RYGDPFYYYMMNV (SEQ ID NO: 2755)
I074H07	1488	143 - 253	167 - 177	193 - 199	232 - 242	1 - 127	26 - 35	50 - 66	99 - 116	GTGYDILTGYYMGSAFDQ (SEQ ID NO: 2800)
I074H08	1489	142 - 254	165 - 178	194 - 200	233 - 243	1 - 126	26 - 35	50 - 66	99 - 115	VSNDILTGWGGYNWFDP (SEQ ID NO: 2955)
I075A07	1490	143 - 253	167 - 177	193 - 199	232 - 242	1 - 127	26 - 35	50 - 66	99 - 116	GTGYDILTGYYMGSAFDQ (SEQ ID NO: 2800)
I075B01	1491	133 - 244	156 - 168	184 - 190	223 - 233	1 - 117	26 - 35	50 - 66	99 - 106	DQGRYLDL (SEQ ID NO: 2175)
I075B04	1492	133 - 247	156 - 169	185 - 191	224 - 236	1 - 117	26 - 35	50 - 66	99 - 106	DQGRYLDL (SEQ ID NO: 2175)
I075B06	1493	140 - 252	163 - 175	191 - 197	230 - 241	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I075B08	1494	143 - 257	166 - 179	195 - 201	234 - 246	1 - 127	26 - 35	50 - 66	99 - 116	GTGYDILTGYYMGSAFDQ (SEQ ID NO: 2800)
I075B09	1495	141 - 252	164 - 176	192 - 198	231 - 241	1 - 125	26 - 35	50 - 66	99 - 114	TYDILTGYYAEYFQH (SEQ ID NO: 2932)
I075B12	1496	140 - 251	163 - 176	192 - 198	231 - 240	1 - 124	26 - 35	50 - 66	99 - 113	SDYDILTGYYWVPV (SEQ ID NO: 2812)
I075C01	1497	147 - 259	170 - 183	199 - 205	238 - 248	1 - 131	26 - 35	50 - 66	99 - 120	GREDDKVKPWPDRYFHYYYMDV (SEQ ID NO: 2835)
I075C05	1498	133 - 244	156 - 168	184 - 190	223 - 233	1 - 117	26 - 35	50 - 66	99 - 106	DQGRYLDL (SEQ ID NO: 2175)
I075D05	1499	143 - 253	168 - 179	195 - 201	234 - 242	1 - 127	26 - 35	50 - 66	99 - 116	GTGYDILTGYYMGSAFDQ (SEQ ID NO: 2897)
I075D07	1500	141 - 252	164 - 176	192 - 198	231 - 241	1 - 125	26 - 35	50 - 66	99 - 114	SYDILTGYPHPLDY (SEQ ID NO: 2853)
I075D08	1501	140 - 251	163 - 175	191 - 197	230 - 240	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I075E01	1502	143 - 253	167 - 177	193 - 199	232 - 242	1 - 127	26 - 35	50 - 66	99 - 116	GTGYDILTGYYMGSAFDQ (SEQ ID NO: 2800)
I075E03	1503	148 - 261	172 - 184	200 - 206	239 - 250	1 - 132	28 - 37	52 - 68	101 - 121	GGGYDILTGYSYPYLYGLDV (SEQ ID NO: 2865)
I075E04	1504	143 - 255	166 - 179	195 - 201	234 - 244	1 - 127	26 - 35	50 - 66	99 - 116	GRGYDVLGTGYFTGSPDY (SEQ ID NO: 2881)
I075E05	1505	140 - 252	163 - 176	192 - 198	231 - 241	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)

I075E10	1506	140 - 252	163 - 176	192 - 198	231 - 241	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I075E11	1507	133 - 244	156 - 168	184 - 190	223 - 233	1 - 117	26 - 35	50 - 66	99 - 106	SGPGWFDP (SEQ ID NO: 2870)
I075E12	1508	142 - 254	165 - 178	194 - 200	233 - 243	1 - 126	26 - 35	50 - 66	99 - 115	TDREFGAKDVTARWGMVDV (SEQ ID NO: 2979)
I075F02	1509	144 - 253	168 - 178	194 - 200	233 - 242	1 - 128	26 - 35	50 - 66	99 - 117	EQGYDILTGYPYEGGWFD (SEQ ID NO: 2834)
I075F04	1510	141 - 251	164 - 176	192 - 198	231 - 240	1 - 125	26 - 37	52 - 67	100 - 114	AGYDILTGYPFYFDS (SEQ ID NO: 2757)
I075F06	1511	144 - 254	168 - 178	194 - 200	233 - 243	1 - 128	26 - 35	50 - 66	99 - 117	GRNYDFTLGTYNFNLGLDY (SEQ ID NO: 2830)
I075F07	1512	140 - 251	163 - 175	191 - 197	230 - 240	1 - 124	26 - 35	50 - 66	99 - 113	ENYDSLTYGYNFYDY (SEQ ID NO: 2971)
I075F08	1513	133 - 244	156 - 168	184 - 190	223 - 233	1 - 117	26 - 35	50 - 66	99 - 106	DQRKAQDI (SEQ ID NO: 2779)
I075F09	1514	145 - 257	169 - 181	197 - 203	236 - 246	1 - 129	26 - 35	50 - 66	99 - 118	LKAPYYDILTYGHLPKWFD (SEQ ID NO: 2953)
I075F10	1515	133 - 243	157 - 167	183 - 189	222 - 232	1 - 117	26 - 35	50 - 66	99 - 106	DQGRYLDL (SEQ ID NO: 2175)
I075F11	1516	133 - 245	156 - 169	185 - 191	224 - 234	1 - 117	26 - 35	50 - 66	99 - 106	DQGRYLDL (SEQ ID NO: 2175)
I075G05	1517	140 - 252	163 - 175	191 - 197	230 - 241	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I075G07	1518	140 - 252	163 - 175	191 - 197	230 - 241	1 - 124	26 - 35	50 - 66	99 - 113	GRYYDMLTRGGYFDY (SEQ ID NO: 2858)
I075G08	1519	140 - 252	163 - 176	192 - 198	231 - 241	1 - 124	26 - 35	50 - 66	99 - 113	RQYDILTYGGYFDY (SEQ ID NO: 2958)
I075G11	1520	141 - 253	164 - 177	193 - 199	232 - 242	1 - 125	26 - 35	50 - 66	99 - 114	TDYDILTYGPMGYFDP (SEQ ID NO: 2173)
I075G12	1521	133 - 245	156 - 169	185 - 191	224 - 234	1 - 117	26 - 35	50 - 66	99 - 106	DQGRYLDL (SEQ ID NO: 2175)
I075H02	1522	143 - 254	166 - 178	194 - 200	233 - 243	1 - 127	26 - 35	50 - 66	99 - 116	GTGYDILTYMGSAFDQ (SEQ ID NO: 2800)
I075H03	1523	133 - 245	156 - 169	185 - 191	224 - 234	1 - 117	26 - 35	50 - 66	99 - 106	DQGRYLDL (SEQ ID NO: 2175)
I075H06	1524	133 - 244	156 - 168	184 - 190	223 - 233	1 - 117	26 - 35	50 - 66	99 - 106	DQGRYLDL (SEQ ID NO: 2175)
I075H08	1525	143 - 254	166 - 179	195 - 201	234 - 243	1 - 127	26 - 35	50 - 66	99 - 116	GSGYDILTYFTGSPLDY (SEQ ID NO: 2766)
I076A01	1526	142 - 253	166 - 176	192 - 198	231 - 242	1 - 126	26 - 35	50 - 66	99 - 115	DRRDDLTGLYDAFDS (SEQ ID NO: 2878)
I076A03	1527	135 - 247	159 - 171	187 - 193	226 - 236	1 - 119	26 - 35	50 - 68	101 - 108	GYDTAMQY (SEQ ID NO: 2951)
I076A06	1528	133 - 245	156 - 168	184 - 190	223 - 234	1 - 117	26 - 35	50 - 66	99 - 106	DQGRYLDL (SEQ ID NO: 2175)
I076A07	1529	139 - 250	162 - 174	190 - 196	229 - 239	1 - 123	26 - 35	50 - 66	99 - 112	DRRDILTSNFGQD (SEQ ID NO: 2913)
I076A08	1530	142 - 253	166 - 176	192 - 198	231 - 242	1 - 126	26 - 35	50 - 66	99 - 115	MGHYDILTYRHYGMDV (SEQ ID NO: 2831)
I076B01	1531	143 - 257	167 - 179	195 - 201	236 - 246	1 - 127	26 - 35	50 - 66	99 - 116	GSGYDILTYFTGSPLDY (SEQ ID NO: 2766)
I076B03	1532	133 - 245	156 - 169	185 - 191	224 - 234	1 - 117	26 - 35	50 - 66	99 - 106	DQGRYLDL (SEQ ID NO: 2175)
I076B07	1533	133 - 243	157 - 167	183 - 189	222 - 232	1 - 117	26 - 35	50 - 66	99 - 106	DQGRYLDL (SEQ ID NO: 2175)
I076B08	1534	141 - 252	166 - 177	193 - 199	232 - 241	1 - 125	26 - 35	50 - 66	99 - 114	PYYDPLTAYTFQYFGN (SEQ ID NO: 2806)
I076C04	1535	140 - 250	164 - 174	190 - 196	229 - 239	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I076C10	1536	140 - 251	163 - 175	191 - 197	230 - 240	1 - 124	26 - 35	50 - 66	99 - 113	GRYYDMLTRGGYFDY (SEQ ID NO: 2858)
I076D01	1537	141 - 252	164 - 176	192 - 198	231 - 241	1 - 125	26 - 35	50 - 66	99 - 114	LDYDILTYGYPGFDY (SEQ ID NO: 2799)
I076D08	1538	140 - 251	163 - 175	191 - 197	230 - 240	1 - 124	26 - 37	52 - 67	100 - 113	RFYDILTYSAFDS (SEQ ID NO: 2756)
I076D11	1539	143 - 255	166 - 179	195 - 201	234 - 244	1 - 127	26 - 35	50 - 66	99 - 116	GTGYDILTYMGSAFDQ (SEQ ID NO: 2800)
I076D12	1540	140 - 250	164 - 174	190 - 196	229 - 239	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I076E04	1541	143 - 252	167 - 177	193 - 199	232 - 241	1 - 127	26 - 35	50 - 66	99 - 116	GTGYDILTYMGSAFDQ (SEQ ID NO: 2800)

I076E07	1542	140 - 251	163 - 175	191 - 197	230 - 240	1 - 124	26 - 35	50 - 66	99 - 113	EYDVLTLFYMDV (SEQ ID NO: 2841)
I076E09	1543	141 - 253	164 - 177	193 - 199	232 - 242	1 - 125	26 - 35	50 - 66	99 - 114	DDRDILTNVLEYFQH (SEQ ID NO: 2868)
I076E11	1544	143 - 254	166 - 179	195 - 201	234 - 243	1 - 127	26 - 35	50 - 66	99 - 116	GTGYDILTGYYMGSAFDQ (SEQ ID NO: 2800)
I076F01	1545	143 - 253	166 - 178	194 - 199	232 - 242	1 - 127	26 - 35	50 - 66	99 - 116	GTGYDILTGYYMGSAFDQ (SEQ ID NO: 2800)
I076F03	1546	140 - 251	163 - 175	191 - 197	230 - 240	1 - 124	26 - 36	51 - 66	99 - 113	GDYDVLTYLRKLDY (SEQ ID NO: 2742)
I076F04	1547	133 - 245	157 - 169	185 - 191	224 - 234	1 - 117	26 - 35	50 - 66	99 - 106	DQGRYDL (SEQ ID NO: 2175)
I076F08	1548	140 - 250	164 - 174	190 - 196	229 - 239	1 - 124	26 - 36	51 - 66	99 - 113	VHYDILTYLWAFDI (SEQ ID NO: 2730)
I076F10	1549	140 - 252	163 - 175	191 - 197	230 - 241	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I076G09	1550	133 - 245	156 - 168	184 - 190	223 - 234	1 - 117	26 - 35	50 - 66	99 - 106	DQGRYDL (SEQ ID NO: 2175)
I076G10	1551	140 - 251	163 - 175	191 - 197	230 - 240	1 - 124	26 - 35	50 - 66	99 - 113	GRYYDMLTRGGYFDY (SEQ ID NO: 2858)
I076G11	1552	143 - 259	166 - 179	195 - 205	240 - 248	1 - 127	26 - 35	50 - 66	99 - 116	GTGYDILTGYYMGSAFDQ (SEQ ID NO: 2800)
I076G12	1553	146 - 257	169 - 181	197 - 203	236 - 246	1 - 130	26 - 35	50 - 66	99 - 119	NGYYDILTYLWDYYYGMDV (SEQ ID NO: 2769)
I076H02	1554	140 - 251	163 - 175	191 - 197	230 - 240	1 - 124	26 - 35	50 - 66	99 - 113	ENYDSLTYNNYFDY (SEQ ID NO: 2971)
I076H04	1555	141 - 251	165 - 175	191 - 197	230 - 240	1 - 125	26 - 35	50 - 66	99 - 114	THYDILTYYSHPLDY (SEQ ID NO: 2863)
I076H05	1556	140 - 251	163 - 175	191 - 197	230 - 240	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I076H06	1557	140 - 252	163 - 176	192 - 198	231 - 241	1 - 124	26 - 35	50 - 66	99 - 113	VPYDILTYWGAFDV (SEQ ID NO: 2827)
I076H09	1558	143 - 256	166 - 179	195 - 201	234 - 245	1 - 127	26 - 35	50 - 66	99 - 116	GSGYDLTYFTGSPLDY (SEQ ID NO: 2766)
I076H10	1559	143 - 256	166 - 179	195 - 201	234 - 245	1 - 127	26 - 35	50 - 66	99 - 116	GSGYDLTYFTGSPLDY (SEQ ID NO: 2766)
I077D06	1560	140 - 250	162 - 175	191 - 197	230 - 239	1 - 124	26 - 35	50 - 66	99 - 113	VYDILTYNLFEDY (SEQ ID NO: 2177)
I078B04	1561	140 - 250	162 - 175	191 - 197	230 - 239	1 - 124	26 - 35	50 - 66	99 - 113	VYDILTYNLFEDY (SEQ ID NO: 2177)
I078E10	1562	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	MEYDILTYGGYFDY (SEQ ID NO: 2179)
I002A01-K	1563	141 - 250	164 - 174	190 - 196	229 - 239	1 - 125	26 - 35	50 - 66	99 - 114	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I002A01-R	1564	141 - 250	164 - 174	190 - 196	229 - 239	1 - 125	26 - 35	50 - 66	99 - 114	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I026C04-K	1565	141 - 250	164 - 176	192 - 198	231 - 239	1 - 125	26 - 35	50 - 66	99 - 114	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I026C04-R	1566	141 - 250	164 - 176	192 - 198	231 - 239	1 - 125	26 - 35	50 - 66	99 - 114	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I067B10	1567	149 - 259	171 - 183	199 - 205	238 - 248	1 - 133	26 - 35	50 - 66	99 - 122	DRGAPNYDILTYYPAPQGVAFDI (SEQ ID NO: 2176)
I068C06	1568	133 - 244	156 - 169	185 - 191	224 - 233	1 - 117	26 - 35	50 - 66	99 - 106	DQGRYDL (SEQ ID NO: 2175)
I075F12	1569	133 - 244	156 - 168	184 - 190	223 - 233	1 - 117	26 - 35	50 - 66	99 - 106	DQGRYDL (SEQ ID NO: 2175)
I003C06	1570	140 - 249	163 - 173	189 - 195	228 - 238	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I025B06	1571	140 - 249	163 - 175	191 - 197	230 - 238	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I025B09	1572	140 - 249	163 - 175	191 - 197	230 - 238	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I026C04	1573	140 - 249	163 - 175	191 - 197	230 - 238	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I027B12	1574	141 - 250	164 - 174	190 - 196	229 - 239	1 - 125	26 - 34	49 - 65	99 - 114	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I030A10	1575	140 - 252	163 - 176	192 - 198	231 - 241	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I064C04	1576	147 - 257	169 - 182	198 - 204	237 - 246	1 - 131	26 - 35	50 - 66	99 - 120	DGRLSYDILTYYYARDYYGMDD (SEQ ID NO: 2188)
I064C07	1577	134 - 241	157 - 167	183 - 189	222 - 230	1 - 118	26 - 35	50 - 66	99 - 107	SEGTIFGVD (SEQ ID NO: 2178)

I065D04	1578	144 - 254	166 - 179	195 - 201	234 - 243	1 - 128	26 - 36	51 - 66	99 - 117	GKGYDILTGYYRDNWFDP (SEQ ID NO: 2181)
I065D08	1579	147 - 257	169 - 182	198 - 204	237 - 246	1 - 131	26 - 35	50 - 66	99 - 120	TPSSVYDILTGYYHYFYSYMDV (SEQ ID NO: 2189)
I065F08	1580	135 - 242	158 - 168	184 - 190	223 - 231	1 - 119	26 - 35	50 - 66	99 - 108	EKSAAGYFDY (SEQ ID NO: 2190)
I067F05	1581	140 - 250	162 - 175	191 - 197	230 - 239	1 - 124	26 - 35	50 - 66	99 - 113	ENYDSL TGYGAFDI (SEQ ID NO: 2185)
I068B04	1582	133 - 244	156 - 168	184 - 190	223 - 233	1 - 117	26 - 35	50 - 66	99 - 106	DQGRYDL (SEQ ID NO: 2175)
I068B08	1583	140 - 252	163 - 175	191 - 197	231 - 241	1 - 124	26 - 34	49 - 65	98 - 113	KLGLSIVGATTGALDM (SEQ ID NO: 2186)
I068C08	1584	142 - 254	165 - 178	194 - 200	233 - 243	1 - 126	26 - 35	50 - 66	99 - 115	EGMNDFINSHHYTMDA (SEQ ID NO: 2182)
I068F03	1585	139 - 251	162 - 175	191 - 197	230 - 240	1 - 123	26 - 35	50 - 66	99 - 112	AGNEYGHTERPADY (SEQ ID NO: 2180)
I069B07	1586	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	MEYDIL TGYGGYFDY (SEQ ID NO: 2179)
I071B03	1587	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPL TGSFDFDI (SEQ ID NO: 2153)
I072B09	1588	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPL TGSFDFDI (SEQ ID NO: 2153)
I073F04	1589	136 - 246	158 - 171	187 - 193	226 - 235	1 - 120	26 - 35	50 - 66	99 - 109	SLATRPLGMDV (SEQ ID NO: 2184)
I074B12	1590	140 - 252	164 - 176	192 - 198	231 - 241	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I075A02	1591	140 - 251	163 - 175	191 - 197	230 - 240	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I075G01	1592	140 - 251	164 - 174	190 - 196	229 - 240	1 - 124	26 - 35	50 - 66	99 - 113	DHFDLTGYFRRLDS (SEQ ID NO: 2187)
I078D02	1593	140 - 250	162 - 175	191 - 197	230 - 239	1 - 124	26 - 35	50 - 66	99 - 113	VYYDIL TGNLFFDY (SEQ ID NO: 2177)
I078D08	1594	144 - 251	165 - 175	191 - 197	230 - 240	1 - 128	26 - 35	50 - 66	99 - 117	DAQSYYDIL TGYQSYAFDI (SEQ ID NO: 2183)
I078H08	1595	140 - 250	162 - 175	191 - 197	230 - 239	1 - 124	26 - 35	50 - 66	99 - 113	VYYDIL TGNLFFDY (SEQ ID NO: 2177)
I064A03	1596	150 - 257	171 - 181	197 - 203	236 - 246	1 - 134	26 - 35	50 - 66	99 - 123	GPSTYYDIL TGYTPYYYYMDV (SEQ ID NO: 3014)
I064B03	1597	145 - 255	167 - 179	195 - 201	234 - 244	1 - 129	26 - 37	52 - 67	100 - 118	HVRDYDIL TGYRGHYFDY (SEQ ID NO: 2167)
I064B05	1598	140 - 250	162 - 174	190 - 196	229 - 239	1 - 124	26 - 35	50 - 66	99 - 111	ERGVTAYGDSFDL (SEQ ID NO: 2985)
I064B11	1599	138 - 248	160 - 173	189 - 195	228 - 237	1 - 122	26 - 35	50 - 66	99 - 111	DRGGLSSFFES (SEQ ID NO: 2985)
I064C02	1600	146 - 256	168 - 180	196 - 202	235 - 245	1 - 130	26 - 35	50 - 66	99 - 119	DEYYDIL TGYQAPYYYYGMDV (SEQ ID NO: 3068)
I064C03	1601	140 - 250	162 - 175	191 - 197	230 - 239	1 - 124	26 - 35	50 - 66	99 - 113	ERGVTAYGDSFDL (SEQ ID NO: 2985)
I064C11	1602	143 - 253	165 - 178	194 - 200	233 - 242	1 - 127	26 - 35	50 - 65	98 - 116	DVTYHDIL TGYAGHEAFDI (SEQ ID NO: 3055)
I064C12	1603	148 - 255	171 - 181	197 - 203	236 - 244	1 - 132	26 - 37	52 - 69	102 - 121	ESGRYDIL TGYSGGGMDV (SEQ ID NO: 3012)
I064D03	1604	146 - 256	168 - 181	197 - 203	236 - 245	1 - 130	26 - 35	50 - 66	99 - 119	DGANYDIL TGYTTTYYGMDV (SEQ ID NO: 3072)
I064D04	1605	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	RSYDIL TGYTYGMDV (SEQ ID NO: 3090)
I064D06	1606	134 - 244	156 - 169	185 - 191	224 - 233	1 - 118	26 - 35	50 - 66	99 - 107	EGSSGYLVG (SEQ ID NO: 2981)
I064E05	1607	146 - 256	168 - 180	196 - 202	235 - 245	1 - 130	26 - 37	52 - 67	100 - 119	KQRGDYDIL TGYQLGYAFDI (SEQ ID NO: 2808)
I064E06	1608	145 - 255	167 - 180	196 - 202	235 - 244	1 - 129	26 - 35	50 - 66	99 - 118	ERPGYDIL TGYPSIYGMVDV (SEQ ID NO: 3053)
I064F07	1609	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPL TGSFDFDI (SEQ ID NO: 2153)
I064F09	1610	147 - 257	169 - 181	197 - 203	236 - 246	1 - 131	26 - 35	50 - 66	99 - 120	DTLGYDIL TGYPPPPYYMDV (SEQ ID NO: 2988)
I064F10	1611	143 - 253	165 - 177	193 - 199	232 - 242	1 - 127	22 - 31	46 - 62	95 - 116	DTLGYDIL TGYPPPPYYMDV (SEQ ID NO: 2988)
I064F11	1612	142 - 252	164 - 177	193 - 199	232 - 241	1 - 126	26 - 35	50 - 65	98 - 115	GRHYDIL TGYNEAFDI (SEQ ID NO: 3031)
I064G01	1613	140 - 250	162 - 175	191 - 197	230 - 239	1 - 124	26 - 35	50 - 66	99 - 113	NYDVL TQSYGMDV (SEQ ID NO: 3077)

I064G04	1614	133 - 243	155 - 167	183 - 189	222 - 232	1 - 117	26 - 35	50 - 66	99 - 106	DNSGTGY (SEQ ID NO: 3084)
I064G08	1615	138 - 245	159 - 169	185 - 191	224 - 234	1 - 122	26 - 35	50 - 66	99 - 111	GGVTAGRSVYFDS (SEQ ID NO: 2990)
I064G10	1616	140 - 250	162 - 175	191 - 197	230 - 239	1 - 124	26 - 35	50 - 66	99 - 113	SPNGDSGYAWGLE (SEQ ID NO: 3085)
I064G11	1617	138 - 248	160 - 173	189 - 195	228 - 237	1 - 122	26 - 35	50 - 65	98 - 111	YFDGSGYVPVSFSY (SEQ ID NO: 3064)
I064G12	1618	139 - 249	161 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 65	98 - 112	VNYDILTGLGYFDY (SEQ ID NO: 3049)
I064H03	1619	143 - 253	165 - 178	194 - 200	233 - 242	1 - 127	26 - 37	52 - 67	100 - 116	SYDILTGRPYTDAFI (SEQ ID NO: 2989)
I064H04	1620	142 - 249	163 - 173	189 - 195	228 - 238	1 - 126	26 - 35	50 - 66	99 - 115	PLGITAVRGAKTDAFGI (SEQ ID NO: 2929)
I064H06	1621	149 - 256	170 - 180	196 - 202	235 - 245	1 - 133	26 - 35	50 - 66	99 - 122	DRGASNYDILTGYYAPAQGVAFDI (SEQ ID NO: 2969)
I065A02	1622	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFI (SEQ ID NO: 2153)
I065A04	1623	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFI (SEQ ID NO: 2153)
I065A06	1624	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFI (SEQ ID NO: 2153)
I065A07	1625	144 - 254	166 - 179	195 - 201	234 - 243	1 - 128	26 - 35	50 - 66	99 - 117	DGGYDILTGYYGYGMDV (SEQ ID NO: 2987)
I065B01	1626	145 - 255	167 - 180	196 - 202	235 - 244	1 - 129	26 - 35	50 - 65	98 - 118	WATYDILTGYRLKDHAGFI (SEQ ID NO: 3017)
I065B05	1627	142 - 252	164 - 177	193 - 199	232 - 241	1 - 126	26 - 35	50 - 66	99 - 115	SPGDDILTGYYKYFDY (SEQ ID NO: 3032)
I065B09	1628	146 - 253	167 - 177	193 - 199	232 - 242	1 - 130	26 - 35	50 - 66	99 - 119	DAGESYDILTGYYVIEGYMDV (SEQ ID NO: 2986)
I065B12	1629	139 - 249	161 - 174	190 - 196	229 - 238	1 - 123	26 - 35	50 - 66	99 - 112	EGAADYLNQYFQH (SEQ ID NO: 2815)
I065C02	1630	136 - 246	158 - 170	186 - 192	225 - 235	1 - 120	26 - 35	50 - 66	99 - 109	EGSWSGLDLDY (SEQ ID NO: 3007)
I065C06	1631	141 - 253	163 - 175	191 - 197	230 - 242	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFI (SEQ ID NO: 2153)
I065C08	1632	141 - 250	163 - 176	192 - 198	231 - 239	1 - 125	26 - 35	50 - 66	99 - 114	VSGYNSGYFESYDMDV (SEQ ID NO: 2732)
I065C10	1633	137 - 247	159 - 172	188 - 194	227 - 236	1 - 121	26 - 35	50 - 66	99 - 110	QGGYDPSPLDV (SEQ ID NO: 3002)
I065D01	1634	142 - 252	164 - 177	193 - 199	232 - 241	1 - 126	26 - 35	50 - 66	99 - 115	DRDYDILTDYSNYYGMDV (SEQ ID NO: 3074)
I065D03	1635	142 - 249	165 - 175	191 - 197	230 - 238	1 - 126	26 - 35	50 - 66	99 - 115	APLYDILTGYYIGGNDY (SEQ ID NO: 3028)
I065D05	1636	143 - 253	165 - 178	194 - 200	233 - 242	1 - 127	26 - 35	50 - 66	99 - 116	DKDYDILTGYYWRDELLDY (SEQ ID NO: 3040)
I065D06	1637	142 - 252	164 - 177	193 - 199	232 - 241	1 - 126	26 - 35	50 - 66	99 - 115	DPNYDILTGYYYYAMDV (SEQ ID NO: 3062)
I065E01	1638	139 - 246	160 - 170	186 - 192	225 - 235	1 - 123	26 - 35	50 - 66	99 - 112	EFQQLARGHGMDV (SEQ ID NO: 3027)
I065E05	1639	137 - 244	158 - 168	184 - 190	223 - 233	1 - 121	26 - 35	50 - 66	99 - 110	AGSSLMYGTDV (SEQ ID NO: 2773)
I065E06	1640	146 - 256	168 - 181	197 - 203	236 - 245	1 - 130	26 - 35	50 - 66	99 - 119	ARGSYDILTGYYRPGDGYFDY (SEQ ID NO: 3043)
I065E08	1641	142 - 249	163 - 173	189 - 195	228 - 238	1 - 126	26 - 35	50 - 66	99 - 115	GLYFEDTNYRHGDAFI (SEQ ID NO: 2790)
I065E09	1642	145 - 255	167 - 179	195 - 201	234 - 244	1 - 129	26 - 35	50 - 65	98 - 118	ERSYYDILTGYSRSGYMDV (SEQ ID NO: 3021)
I065E12	1643	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFI (SEQ ID NO: 2153)
I065F04	1644	140 - 250	162 - 175	191 - 197	230 - 239	1 - 124	26 - 35	50 - 66	99 - 113	ERGVVTA YGGDSFDL (SEQ ID NO: 2985)
I065F05	1645	140 - 250	162 - 175	191 - 197	230 - 239	1 - 124	26 - 35	50 - 65	98 - 113	RYSDALTGYSGLGAFDV (SEQ ID NO: 3018)
I065F07	1646	145 - 252	166 - 176	192 - 198	231 - 241	1 - 129	26 - 38	53 - 69	102 - 118	GAYYDILTGYYPYGMDV (SEQ ID NO: 2860)
I065F09	1647	143 - 250	164 - 174	190 - 196	229 - 239	1 - 127	26 - 35	50 - 66	99 - 116	DYPIDVLTGRRTKNWFDP (SEQ ID NO: 3013)
I065F12	1648	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	DQVDRLLMQYNYMDA (SEQ ID NO: 3047)
I065G01	1649	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFI (SEQ ID NO: 2153)

I065G09	1650	143 - 253	165 - 178	194 - 200	233 - 242	1 - 127	26 - 35	50 - 68	101 - 116	DAYDILTGWVYGM DV (SEQ ID NO: 3030)
I065G10	1651	140 - 247	161 - 171	187 - 193	226 - 236	1 - 124	26 - 36	51 - 66	99 - 113	FRYDILTGYYDM DV (SEQ ID NO: 2983)
I065H05	1652	140 - 247	161 - 171	187 - 193	226 - 236	1 - 124	26 - 35	50 - 66	99 - 113	EYDILTGYSAGFDI (SEQ ID NO: 2984)
I065H07	1653	138 - 248	160 - 173	189 - 195	228 - 237	1 - 122	26 - 35	50 - 66	99 - 111	TRMDVLTRYYSDF (SEQ ID NO: 2750)
I066A05	1654	137 - 247	159 - 172	188 - 194	227 - 236	1 - 121	26 - 35	50 - 66	99 - 110	AGSLMTYGT DV (SEQ ID NO: 2773)
I066A06	1655	139 - 246	160 - 170	186 - 192	225 - 235	1 - 123	26 - 35	50 - 66	99 - 112	EGAADYLNQYFQH (SEQ ID NO: 2815)
I066A12	1656	142 - 252	164 - 177	193 - 199	232 - 241	1 - 126	26 - 35	50 - 66	99 - 115	DTRVIGIQLW ERGA FDM (SEQ ID NO: 3080)
I066B05	1657	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSF DGF DI (SEQ ID NO: 2153)
I066B11	1658	142 - 252	164 - 177	193 - 199	232 - 241	1 - 126	26 - 35	50 - 66	99 - 115	PLGITAVRGA KTDA FGI (SEQ ID NO: 2929)
I066C06	1659	144 - 254	166 - 178	194 - 200	233 - 243	1 - 128	26 - 35	50 - 65	98 - 117	GRRYDILTGYS LGRGEM DV (SEQ ID NO: 3009)
I066C10	1660	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSF DGF DI (SEQ ID NO: 2153)
I066D02	1661	137 - 247	159 - 172	188 - 194	227 - 236	1 - 121	26 - 35	50 - 66	99 - 110	AGTSLMNYGT DV (SEQ ID NO: 3048)
I066D07	1662	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	GPYDVL TGYS LSGNFDY (SEQ ID NO: 2992)
I066E01	1663	137 - 247	159 - 172	188 - 194	227 - 236	1 - 121	26 - 35	50 - 66	99 - 110	QGGQYDSPFDV (SEQ ID NO: 3001)
I066E03	1664	149 - 259	171 - 184	200 - 206	239 - 248	1 - 133	26 - 35	50 - 66	99 - 122	GEKARYYDIL TGYS AWGGYYMDV (SEQ ID NO: 3045)
I066E04	1665	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	LNLEKTVIRGFGYFDL (SEQ ID NO: 3081)
I066E05	1666	142 - 252	164 - 177	193 - 199	232 - 241	1 - 126	26 - 35	50 - 66	99 - 115	VGGYDIL TGYYLRGM DV (SEQ ID NO: 2997)
I066E07	1667	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSF DGF DI (SEQ ID NO: 2153)
I066E09	1668	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSF DGF DI (SEQ ID NO: 2153)
I066F01	1669	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	SPYDIL TGYYVYNGVDV (SEQ ID NO: 3058)
I066F03	1670	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSF DGF DI (SEQ ID NO: 2153)
I066F04	1671	141 - 251	163 - 175	191 - 197	230 - 240	1 - 125	26 - 35	50 - 66	99 - 114	VAAAGARTLG YFGMDV (SEQ ID NO: 3071)
I066F07	1672	143 - 253	165 - 178	194 - 200	233 - 242	1 - 127	26 - 35	50 - 66	99 - 116	DVSGHDIL TGYSRYFDV (SEQ ID NO: 2795)
I066F08	1673	144 - 254	166 - 179	195 - 201	234 - 243	1 - 128	26 - 35	50 - 66	99 - 117	SPMYDRL TGYP SGYFDS (SEQ ID NO: 3036)
I066F11	1674	142 - 252	164 - 177	193 - 199	232 - 241	1 - 126	26 - 35	50 - 66	99 - 115	GAYYDIL TGYP PYGM DV (SEQ ID NO: 2860)
I066F12	1675	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	GPSSAGTIGLGSF DP (SEQ ID NO: 3005)
I066G06	1676	143 - 250	164 - 174	190 - 196	229 - 239	1 - 127	26 - 35	50 - 66	99 - 116	ETRKYTSSPPYNY YMDV (SEQ ID NO: 2736)
I066G07	1677	133 - 243	155 - 168	184 - 190	223 - 232	1 - 117	26 - 30	45 - 61	94 - 106	DQFSVGRHAFDL (SEQ ID NO: 3054)
I066H02	1678	135 - 242	156 - 166	182 - 188	221 - 231	1 - 119	26 - 35	50 - 66	99 - 108	GMGDHYGM DV (SEQ ID NO: 2161)
I067A02	1679	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSF DGF DI (SEQ ID NO: 2153)
I067A03	1680	137 - 247	159 - 172	188 - 194	227 - 236	1 - 121	26 - 35	50 - 66	99 - 110	AGSLMTYGT DV (SEQ ID NO: 2773)
I067A06	1681	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSF DGF DI (SEQ ID NO: 2153)
I067A08	1682	137 - 247	159 - 171	187 - 193	226 - 236	1 - 121	26 - 35	50 - 66	99 - 110	AGSLMTYGT DV (SEQ ID NO: 2773)
I067A10	1683	140 - 250	162 - 175	191 - 197	230 - 239	1 - 124	26 - 35	50 - 66	99 - 113	ERGVVTAYGGDSFDL (SEQ ID NO: 2985)
I067B03	1684	142 - 253	164 - 177	193 - 199	232 - 242	1 - 126	26 - 35	50 - 66	99 - 115	PLGITAVRGA KTDA FGI (SEQ ID NO: 2929)
I067B04	1685	137 - 247	159 - 172	188 - 194	227 - 236	1 - 121	26 - 35	50 - 66	99 - 110	AGSLMTYGT DV (SEQ ID NO: 2773)

I067C03	1686	133 - 244	156 - 169	185 - 191	224 - 233	1 - 117	26 - 35	50 - 66	99 - 106	DWGHWFDP (SEQ ID NO: 2982)
I067C05	1687	137 - 247	159 - 172	188 - 194	227 - 236	1 - 121	26 - 35	50 - 66	99 - 110	SGSSLMTYGIDV (SEQ ID NO: 3015)
I067C07	1688	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	EPYDILTGYYGSYFDY (SEQ ID NO: 3041)
I067C10	1689	137 - 247	159 - 172	188 - 194	227 - 236	1 - 121	26 - 35	50 - 66	99 - 110	AGSSLMTYGTDV (SEQ ID NO: 2773)
I067C12	1690	142 - 252	164 - 177	193 - 199	232 - 241	1 - 126	26 - 35	50 - 66	99 - 115	TYDILTGYSGGAFDY (SEQ ID NO: 3024)
I067D01	1691	136 - 246	158 - 171	187 - 193	226 - 235	1 - 120	26 - 35	50 - 66	99 - 109	GSRRGVTPDL (SEQ ID NO: 3020)
I067D03	1692	137 - 244	158 - 168	184 - 190	223 - 233	1 - 121	26 - 35	50 - 66	99 - 110	AGSSLMTYGTDV (SEQ ID NO: 2773)
I067D05	1693	146 - 256	168 - 180	196 - 202	235 - 245	1 - 130	26 - 35	50 - 66	99 - 119	ECSSCPARQPPYYQYMDV (SEQ ID NO: 2993)
I067D06	1694	137 - 244	158 - 168	184 - 190	223 - 233	1 - 121	26 - 35	50 - 66	99 - 110	AGSSLMTYGTDV (SEQ ID NO: 2773)
I067D09	1695	142 - 252	164 - 177	193 - 199	232 - 241	1 - 126	26 - 35	50 - 66	99 - 115	GAYYDILTGYYPYGMDV (SEQ ID NO: 2860)
I067D12	1696	137 - 247	159 - 172	188 - 194	227 - 236	1 - 121	26 - 35	50 - 66	99 - 110	QGGYDPSPLDV (SEQ ID NO: 3002)
I067E02	1697	137 - 247	159 - 172	188 - 194	227 - 236	1 - 121	26 - 35	50 - 66	99 - 110	AGSSLMTYGTDV (SEQ ID NO: 2773)
I067E04	1698	142 - 252	164 - 176	192 - 198	231 - 241	1 - 126	26 - 35	50 - 66	99 - 115	GAYYDILTGYYPYGMDV (SEQ ID NO: 2860)
I067E05	1699	144 - 254	166 - 179	195 - 201	234 - 243	1 - 128	26 - 35	50 - 66	99 - 117	DYRNYDILTHPPYYGMDV (SEQ ID NO: 2996)
I067F01	1700	141 - 248	164 - 174	190 - 196	229 - 237	1 - 125	26 - 35	50 - 66	99 - 114	QHYDILTGYSQEPDI (SEQ ID NO: 3022)
I067F03	1701	144 - 254	166 - 179	195 - 201	234 - 243	1 - 128	26 - 35	50 - 66	99 - 117	DQTYDILTGHHYYGMDV (SEQ ID NO: 3087)
I067F04	1702	139 - 246	160 - 170	186 - 192	225 - 235	1 - 123	26 - 35	50 - 66	99 - 112	EGAADYLNQYFQH (SEQ ID NO: 2815)
I067F08	1703	140 - 247	161 - 171	187 - 193	226 - 236	1 - 124	26 - 35	50 - 66	99 - 113	LGYYDILTGYSRDDY (SEQ ID NO: 3029)
I067F10	1704	137 - 247	159 - 172	188 - 194	227 - 236	1 - 121	26 - 35	50 - 66	99 - 110	AGSSLMAYGTDV (SEQ ID NO: 3016)
I067F11	1705	140 - 248	161 - 171	187 - 193	226 - 237	1 - 124	26 - 35	50 - 66	99 - 113	ENYDPLTGYYGAFDI (SEQ ID NO: 2772)
I067G01	1706	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDFDI (SEQ ID NO: 2153)
I067G09	1707	137 - 247	159 - 171	187 - 193	226 - 236	1 - 121	26 - 35	50 - 66	99 - 110	AGSSLMTYGTDV (SEQ ID NO: 2773)
I067H07	1708	144 - 251	165 - 175	191 - 197	230 - 240	1 - 128	26 - 35	50 - 66	99 - 117	GGLYDILTGTPATDDAFDI (SEQ ID NO: 3035)
I068A07	1709	142 - 254	165 - 178	194 - 200	233 - 243	1 - 126	26 - 35	50 - 66	99 - 115	TDRFGAKDVTARWGMDV (SEQ ID NO: 2979)
I068E05	1710	147 - 257	170 - 183	199 - 205	238 - 246	1 - 131	26 - 35	50 - 66	99 - 120	GREDDKVKPWDRYYHHYYMDV (SEQ ID NO: 2809)
I068E08	1711	133 - 247	157 - 169	185 - 193	226 - 236	1 - 117	26 - 35	50 - 66	99 - 106	DQGRYLDL (SEQ ID NO: 2175)
I068E11	1712	140 - 251	163 - 176	192 - 198	231 - 240	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I068F04	1713	141 - 252	164 - 176	192 - 198	231 - 241	1 - 125	26 - 35	50 - 66	99 - 114	ELGHRGGYWYSPYNV (SEQ ID NO: 2838)
I068G05	1714	135 - 245	159 - 169	185 - 191	224 - 234	1 - 119	26 - 35	50 - 66	98 - 108	KNMGASAAADF (SEQ ID NO: 3042)
I068G06	1715	139 - 250	162 - 174	190 - 196	229 - 239	1 - 123	26 - 35	50 - 66	99 - 112	RYGDPFYYYYYMNV (SEQ ID NO: 2755)
I068G11	1716	146 - 258	169 - 182	198 - 204	237 - 247	1 - 130	26 - 35	50 - 66	99 - 119	ESGSHYDLLTGLLVAANGFDV (SEQ ID NO: 3044)
I069A09	1717	141 - 248	164 - 174	190 - 196	229 - 237	1 - 125	26 - 35	50 - 66	99 - 114	MEYDILTGYYGGYFDY (SEQ ID NO: 2179)
I069A10	1718	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	MEYDILTGYYGGYFDY (SEQ ID NO: 2179)
I069B06	1719	141 - 248	164 - 174	190 - 196	229 - 237	1 - 125	26 - 35	50 - 66	99 - 114	MEYDILTGYYGGYFDY (SEQ ID NO: 2179)
I069B09	1720	139 - 249	161 - 174	190 - 196	229 - 238	1 - 123	26 - 35	50 - 66	99 - 112	PYYDILTGYYFAFDI (SEQ ID NO: 3026)
I069B12	1721	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	MEYDILTGYYGGYFDY (SEQ ID NO: 2179)

I069C06	1722	143 - 250	164 - 174	190 - 196	229 - 239	1 - 127	26 - 35	50 - 66	99 - 116	VLPHYDILTGYSQNWFDP (SEQ ID NO: 3000)
I069C09	1723	143 - 250	164 - 174	190 - 196	229 - 239	1 - 127	26 - 35	50 - 66	99 - 116	VLPHYDILTGYSQNWFDP (SEQ ID NO: 3000)
I069D03	1724	142 - 249	163 - 173	189 - 195	228 - 238	1 - 126	26 - 35	50 - 66	99 - 115	DGYDILTGYSYGGMDV (SEQ ID NO: 2135)
I069E09	1725	142 - 249	163 - 173	189 - 195	228 - 238	1 - 126	26 - 35	50 - 66	99 - 115	DGYDILTGYSYGGMDV (SEQ ID NO: 2135)
I069E11	1726	140 - 247	161 - 171	187 - 193	226 - 236	1 - 124	26 - 35	50 - 66	99 - 113	VYYDILTGYNLFDDY (SEQ ID NO: 2177)
I069F05	1727	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	MEYDILTGYYGGYFDY (SEQ ID NO: 2179)
I069F07	1728	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	MEYDILTGYYGGYFDY (SEQ ID NO: 2179)
I069F12	1729	140 - 247	161 - 171	187 - 193	226 - 236	1 - 124	26 - 35	50 - 66	99 - 113	GYYDILTGYYDAFDI (SEQ ID NO: 3051)
I069G06	1730	142 - 249	163 - 173	189 - 195	228 - 238	1 - 126	26 - 35	50 - 66	99 - 115	DGYDILTGYSYGGMDV (SEQ ID NO: 3059)
I069G08	1731	145 - 252	166 - 176	192 - 198	231 - 241	1 - 129	26 - 35	50 - 66	99 - 118	DRLEYDILTGYYGGMDV (SEQ ID NO: 3039)
I069G11	1732	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	MEYDILTGYYGGYFDY (SEQ ID NO: 2179)
I070A03	1733	141 - 248	164 - 174	190 - 196	229 - 239	1 - 125	26 - 35	50 - 66	99 - 114	MEYDILTGYYGGYFDY (SEQ ID NO: 2179)
I070A09	1734	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	MEYDILTGYYGGYFDY (SEQ ID NO: 2179)
I070B01	1735	144 - 254	166 - 179	195 - 201	234 - 243	1 - 128	26 - 35	50 - 66	99 - 117	SQSDYDILTGYYGGMDV (SEQ ID NO: 3038)
I070B05	1736	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	MEYDILTGYYGGYFDY (SEQ ID NO: 2179)
I070D03	1737	141 - 248	164 - 174	190 - 196	229 - 239	1 - 125	26 - 35	50 - 66	99 - 114	MEYDILTSYGGYFDY (SEQ ID NO: 3034)
I070D04	1738	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 117	SQSDYDILTGYYGGMDV (SEQ ID NO: 3038)
I070E01	1739	144 - 254	166 - 179	195 - 201	234 - 243	1 - 128	26 - 35	50 - 66	99 - 117	SQSDYDILTGYYGGMDV (SEQ ID NO: 3038)
I070F01	1740	144 - 251	165 - 175	191 - 197	230 - 240	1 - 125	26 - 35	50 - 66	99 - 117	SQSNYDILTGYYGGMDV (SEQ ID NO: 3067)
I070G10	1741	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	MEYDILTGYYGGYFDY (SEQ ID NO: 2179)
I071A06	1742	135 - 242	156 - 166	182 - 188	221 - 231	1 - 119	26 - 35	50 - 66	99 - 108	GMGDHYGMDV (SEQ ID NO: 2161)
I071B02	1743	135 - 245	157 - 170	186 - 192	225 - 234	1 - 119	26 - 35	50 - 66	99 - 108	GMGDHYGMDV (SEQ ID NO: 2161)
I071D02	1744	137 - 247	159 - 172	188 - 194	227 - 236	1 - 121	26 - 35	50 - 66	99 - 110	AGTSLMNYGTDV (SEQ ID NO: 3048)
I071D08	1745	146 - 256	168 - 181	197 - 203	236 - 245	1 - 130	26 - 37	52 - 66	99 - 119	VPYYDTSGGYLGEYYGMDV (SEQ ID NO: 3010)
I071F01	1746	137 - 247	159 - 172	188 - 194	227 - 236	1 - 121	26 - 35	50 - 66	99 - 110	AGTSLMNYGTDV (SEQ ID NO: 3048)
I071G09	1747	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I072A01	1748	139 - 249	161 - 174	190 - 196	229 - 238	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLLPHYGMDV (SEQ ID NO: 2133)
I072A09	1749	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I072B02	1750	135 - 245	157 - 170	186 - 192	225 - 234	1 - 119	26 - 35	50 - 66	99 - 108	GMGDHYGMDV (SEQ ID NO: 2161)
I072B10	1751	137 - 247	159 - 172	188 - 194	227 - 236	1 - 121	26 - 35	50 - 66	99 - 110	AGSSLMTYGTDV (SEQ ID NO: 2773)
I072B11	1752	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I072B12	1753	140 - 249	162 - 173	189 - 195	228 - 238	1 - 124	26 - 35	50 - 66	99 - 113	ENYDYLTYGGYAFDI (SEQ ID NO: 2995)
I072C05	1754	135 - 245	157 - 169	185 - 191	224 - 234	1 - 119	26 - 35	50 - 66	99 - 108	GMGDHYGMDV (SEQ ID NO: 2161)
I072C10	1755	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I072D01	1756	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I072D05	1757	135 - 245	157 - 169	185 - 191	224 - 234	1 - 119	26 - 35	50 - 66	99 - 108	GMGDHYGMDV (SEQ ID NO: 2161)

I072E01	1758	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I072E04	1759	144 - 254	166 - 179	195 - 201	234 - 243	1 - 128	26 - 35	50 - 66	99 - 117	EGSYDILTGYYVGVGRMDV (SEQ ID NO: 2171)
I072E05	1760	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I072E06	1761	135 - 242	156 - 166	182 - 188	221 - 231	1 - 119	26 - 35	50 - 66	99 - 108	GMGDHYGMDV (SEQ ID NO: 2161)
I072F03	1762	135 - 242	156 - 166	182 - 188	221 - 231	1 - 119	26 - 35	50 - 66	99 - 108	GMGDHYGMDV (SEQ ID NO: 2161)
I072F07	1763	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I072F11	1764	140 - 247	161 - 171	187 - 193	226 - 236	1 - 124	26 - 35	50 - 66	99 - 113	DEYDILTGLQGMVDV (SEQ ID NO: 2883)
I072G03	1765	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I072G04	1766	137 - 247	159 - 171	187 - 193	226 - 236	1 - 121	26 - 35	50 - 68	101 - 110	RDILTFYDS (SEQ ID NO: 2933)
I072G05	1767	137 - 247	159 - 171	187 - 193	226 - 236	1 - 121	26 - 35	50 - 66	99 - 110	GYRNDWYGAFEI (SEQ ID NO: 3079)
I072G09	1768	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I072H03	1769	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I072H07	1770	137 - 247	159 - 172	188 - 194	227 - 236	1 - 121	26 - 35	50 - 66	99 - 110	AGTSLMNYGMDV (SEQ ID NO: 3070)
I073A02	1771	141 - 248	164 - 174	190 - 196	229 - 237	1 - 125	26 - 35	50 - 66	99 - 114	GPYDILTGYYRDAFDI (SEQ ID NO: 2998)
I073A03	1772	142 - 252	164 - 177	193 - 199	232 - 241	1 - 126	26 - 35	50 - 66	99 - 115	THYDILTGYYTADAFDI (SEQ ID NO: 3019)
I073A04	1773	148 - 258	170 - 183	199 - 205	238 - 247	1 - 132	26 - 35	50 - 66	99 - 121	VQMDSEYYDILLTGINVGPPYFDY (SEQ ID NO: 2132)
I073A05	1774	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I073A06	1775	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I073A09	1776	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I073A10	1777	146 - 253	167 - 177	193 - 199	232 - 242	1 - 130	26 - 35	50 - 66	99 - 119	GDFGDYDILTGYYPPVYGMVDV (SEQ ID NO: 3082)
I073A11	1778	141 - 248	164 - 174	190 - 196	229 - 237	1 - 125	26 - 35	50 - 66	99 - 114	SYDILTGYYPFGMVDV (SEQ ID NO: 3004)
I073B02	1779	144 - 254	166 - 179	195 - 201	234 - 243	1 - 128	26 - 35	50 - 66	99 - 117	DLWYYDILTGYYLDDAFDI (SEQ ID NO: 2999)
I073B05	1780	144 - 254	166 - 179	195 - 201	234 - 243	1 - 128	26 - 35	50 - 66	99 - 117	DLWYYDILTGYYLDDAFDI (SEQ ID NO: 2999)
I073B06	1781	139 - 246	160 - 170	186 - 192	225 - 235	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLFPHYGMDV (SEQ ID NO: 2133)
I073B07	1782	138 - 248	160 - 173	189 - 195	228 - 237	1 - 122	26 - 35	50 - 66	99 - 111	TRMDVLTYYSD (SEQ ID NO: 2750)
I073B08	1783	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I073B11	1784	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I073C01	1785	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	GYHDTLTSYNNWFDP (SEQ ID NO: 3006)
I073C02	1786	148 - 255	169 - 179	195 - 201	234 - 244	1 - 132	26 - 35	50 - 66	99 - 121	AQMDSEYYDILLTGINVGPPYFDY (SEQ ID NO: 3076)
I073C04	1787	141 - 252	164 - 177	193 - 199	232 - 241	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I073C07	1788	134 - 241	155 - 165	181 - 187	220 - 230	1 - 118	26 - 35	50 - 66	99 - 107	GMGDHYMDV (SEQ ID NO: 3008)
I073C08	1789	142 - 252	164 - 177	193 - 199	232 - 241	1 - 126	26 - 35	50 - 66	99 - 115	EMGYDILTGYYLNMYMDV (SEQ ID NO: 2862)
I073C09	1790	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	QHYDILTGYSQEPFDI (SEQ ID NO: 3022)
I073C11	1791	146 - 256	168 - 181	197 - 203	236 - 245	1 - 130	26 - 35	50 - 68	101 - 119	FNPTYDILTGYYIGGYFQH (SEQ ID NO: 2155)
I073C12	1792	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I073D01	1793	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)

I073D03	1794	135 - 245	157 - 169	185 - 191	224 - 234	1 - 119	26 - 35	50 - 66	99 - 108	GMGDHYGMDV (SEQ ID NO: 2161)
I073D06	1795	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I073D08	1796	144 - 254	166 - 179	195 - 201	234 - 243	1 - 128	26 - 35	50 - 66	99 - 117	EVRYDILLTRSYLAGPLDN (SEQ ID NO: 2751)
I073D10	1797	140 - 250	162 - 175	191 - 197	230 - 239	1 - 124	26 - 35	50 - 68	101 - 113	QYYDILTGVELDI (SEQ ID NO: 3073)
I073D11	1798	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I073E01	1799	148 - 258	170 - 183	199 - 205	238 - 247	1 - 132	26 - 37	52 - 69	102 - 121	EGAHYDILTGHNYYHYGMDV (SEQ ID NO: 2747)
I073E02	1800	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I073E03	1801	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 3003)
I073E05	1802	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	QHYDILTGYSQEPFDI (SEQ ID NO: 3022)
I073E06	1803	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I073E08	1804	140 - 250	162 - 175	191 - 197	230 - 239	1 - 124	26 - 35	50 - 66	99 - 113	ENYDILTGYYGAFDI (SEQ ID NO: 2772)
I073F01	1805	141 - 251	163 - 175	191 - 197	230 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I073F02	1806	141 - 251	163 - 175	191 - 197	230 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I073F03	1807	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I073F05	1808	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I073F07	1809	141 - 251	163 - 175	191 - 197	230 - 240	1 - 125	26 - 35	50 - 66	99 - 114	GEYDILTGYPYWFYDL (SEQ ID NO: 3023)
I073F09	1810	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I073F11	1811	141 - 251	163 - 175	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I073F12	1812	141 - 251	163 - 175	191 - 197	230 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I073G03	1813	143 - 253	165 - 178	194 - 200	233 - 242	1 - 127	26 - 35	50 - 65	98 - 116	DGSYDILTGYYIDNVMV (SEQ ID NO: 2154)
I073G04	1814	143 - 253	165 - 178	194 - 200	233 - 242	1 - 127	26 - 35	50 - 65	98 - 116	GEGYDILTGYLRYGMDV (SEQ ID NO: 3037)
I073G05	1815	135 - 245	157 - 169	185 - 191	224 - 234	1 - 119	26 - 35	50 - 66	99 - 108	GMGDHYGMDV (SEQ ID NO: 2161)
I073G06	1816	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I073G07	1817	142 - 249	163 - 173	189 - 195	228 - 238	1 - 126	26 - 35	50 - 66	99 - 115	GYYDILTGISLGMV (SEQ ID NO: 3063)
I073G08	1818	139 - 246	160 - 170	186 - 192	225 - 235	1 - 123	26 - 35	50 - 66	99 - 112	SRDLLFPHYGMDV (SEQ ID NO: 2133)
I073G09	1819	145 - 255	167 - 180	196 - 202	235 - 244	1 - 129	26 - 35	50 - 66	99 - 118	DRGHYDILTGYYIEPSGFDY (SEQ ID NO: 3061)
I073G10	1820	135 - 245	157 - 170	186 - 192	225 - 234	1 - 119	26 - 35	50 - 66	99 - 108	GPGVIGNYDY (SEQ ID NO: 2749)
I073G12	1821	142 - 252	164 - 177	193 - 199	232 - 241	1 - 126	26 - 35	50 - 68	101 - 115	GGMIRAREDYVMV (SEQ ID NO: 3083)
I073H01	1822	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I073H03	1823	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I073H05	1824	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I073H06	1825	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I073H07	1826	138 - 245	159 - 169	185 - 191	224 - 234	1 - 122	26 - 35	50 - 66	99 - 111	TYDILTGYYFEDY (SEQ ID NO: 3056)
I073H08	1827	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	ATYDPLTGYSFDGFDI (SEQ ID NO: 2153)
I074A05	1828	143 - 255	166 - 179	195 - 201	234 - 244	1 - 127	26 - 35	50 - 66	99 - 116	LPPYDMLTGYYVGGGMDV (SEQ ID NO: 3050)
I074A06	1829	143 - 253	167 - 177	193 - 199	232 - 242	1 - 127	26 - 35	50 - 66	99 - 116	AKPYDIFSRGSDADAFDV (SEQ ID NO: 3065)

I074B03	1830	133 - 242	156 - 166	182 - 188	221 - 231	1 - 117	26 - 35	50 - 66	99 - 106	DQGRYDL (SEQ ID NO: 2175)
I074B11	1831	139 - 251	162 - 175	191 - 197	230 - 240	1 - 123	26 - 35	50 - 66	99 - 112	RYGDPFYYYMNV (SEQ ID NO: 2755)
I074C07	1832	140 - 251	163 - 175	191 - 197	230 - 240	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I074D03	1833	141 - 251	165 - 175	191 - 197	230 - 240	1 - 125	26 - 35	50 - 66	99 - 114	GGYDILTQYPAEFFHP (SEQ ID NO: 2764)
I074D04	1834	133 - 246	156 - 169	185 - 191	224 - 235	1 - 117	26 - 35	50 - 66	99 - 106	DQGRYDL (SEQ ID NO: 2175)
I074D05	1835	143 - 253	167 - 177	193 - 199	232 - 242	1 - 127	26 - 35	50 - 66	99 - 116	DRYYDILTKGDYYYGMDV (SEQ ID NO: 3060)
I074D07	1836	150 - 262	173 - 186	202 - 208	241 - 251	1 - 134	26 - 35	50 - 66	99 - 123	VQGETYYDILTGYWGPKRDLYGMDV (SEQ ID NO: 3069)
I074D08	1837	140 - 251	163 - 175	191 - 197	230 - 240	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVVATTGALDM (SEQ ID NO: 2980)
I074D11	1838	138 - 249	161 - 174	190 - 196	229 - 238	1 - 122	26 - 35	50 - 66	99 - 111	ESEGDDYTNFGY (SEQ ID NO: 2991)
I074E05	1839	133 - 245	156 - 169	185 - 191	224 - 234	1 - 117	26 - 35	50 - 66	99 - 106	DQGRYDL (SEQ ID NO: 2175)
I074E07	1840	140 - 251	163 - 175	191 - 197	230 - 240	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I074E09	1841	146 - 258	169 - 182	198 - 204	237 - 247	1 - 130	26 - 35	50 - 68	101 - 119	DPGNYDILTGYYYYGMDV (SEQ ID NO: 2935)
I074E11	1842	137 - 244	160 - 170	186 - 192	225 - 233	1 - 121	26 - 35	50 - 66	99 - 110	VRLPHHYFMV (SEQ ID NO: 3075)
I074H05	1843	142 - 254	166 - 178	194 - 200	233 - 243	1 - 126	26 - 35	50 - 66	99 - 115	ESSITVNPPYFYGMDV (SEQ ID NO: 3025)
I075A03	1844	133 - 242	158 - 168	184 - 190	223 - 231	1 - 117	26 - 35	50 - 66	99 - 106	DQGRYDL (SEQ ID NO: 2175)
I075A10	1845	133 - 244	157 - 169	185 - 191	224 - 233	1 - 117	26 - 35	50 - 66	99 - 106	DQGRYDL (SEQ ID NO: 2175)
I075B07	1846	143 - 254	166 - 178	194 - 200	233 - 243	1 - 127	26 - 35	50 - 66	99 - 116	SPEGDYQPLSSNYNWLDP (SEQ ID NO: 3011)
I075D11	1847	133 - 246	156 - 169	185 - 191	224 - 235	1 - 117	26 - 36	51 - 66	99 - 106	GKEGYNDN (SEQ ID NO: 3089)
I075D12	1848	143 - 253	167 - 177	193 - 199	232 - 242	1 - 127	26 - 35	50 - 66	99 - 116	GSGYDLTGYFTGSPLDY (SEQ ID NO: 2766)
I075G02	1849	143 - 255	166 - 179	195 - 201	234 - 244	1 - 127	26 - 35	50 - 66	99 - 116	SPEGDYQPLSSNYNWLDP (SEQ ID NO: 3011)
I075G09	1850	142 - 253	165 - 177	193 - 199	232 - 242	1 - 126	26 - 35	50 - 66	99 - 115	MGYDILTGYRHYGMDV (SEQ ID NO: 2831)
I075G10	1851	138 - 250	162 - 174	190 - 196	229 - 239	1 - 122	26 - 35	50 - 66	99 - 111	GNYDILTYPHDL (SEQ ID NO: 3086)
I075H05	1852	141 - 252	164 - 176	192 - 198	231 - 241	1 - 125	26 - 35	50 - 66	99 - 114	SYDILTGYVHTPLDY (SEQ ID NO: 2853)
I075H07	1853	143 - 253	167 - 177	193 - 199	232 - 242	1 - 127	26 - 35	50 - 66	99 - 116	GSGYDLTGYFTGSPLDY (SEQ ID NO: 2766)
I076A11	1854	141 - 254	164 - 177	193 - 199	232 - 243	1 - 125	26 - 35	50 - 66	99 - 114	DDRDILTNYLEYFQH (SEQ ID NO: 2868)
I076A12	1855	143 - 256	166 - 178	194 - 200	233 - 245	1 - 127	26 - 35	50 - 66	99 - 116	GSGYDVLTYFTGSPLDY (SEQ ID NO: 3057)
I076B06	1856	140 - 249	164 - 174	190 - 196	229 - 238	1 - 127	26 - 35	50 - 66	99 - 113	GRYDILTGYFTSFDY (SEQ ID NO: 3066)
I076B10	1857	141 - 254	164 - 177	193 - 199	232 - 243	1 - 125	26 - 35	50 - 66	99 - 114	DDRDILTNYLEYFQH (SEQ ID NO: 2868)
I076B12	1858	143 - 253	167 - 177	193 - 199	232 - 242	1 - 127	26 - 35	50 - 66	99 - 116	GTGYDILTGYVMGSAFDQ (SEQ ID NO: 2800)
I076C06	1859	142 - 253	165 - 177	193 - 199	232 - 242	1 - 126	26 - 35	50 - 66	99 - 115	MGYDILTGYRHYGMDV (SEQ ID NO: 2831)
I076C11	1860	133 - 245	156 - 168	184 - 190	223 - 234	1 - 117	26 - 35	50 - 66	99 - 106	DQGRYDL (SEQ ID NO: 2175)
I076D06	1861	140 - 252	163 - 176	192 - 198	231 - 241	1 - 124	26 - 34	49 - 65	98 - 113	ELGLSIVGATTGALDM (SEQ ID NO: 2174)
I076E05	1862	143 - 255	166 - 179	195 - 201	234 - 244	1 - 127	26 - 35	50 - 66	99 - 116	GTGYDILTGYVMGSAFDQ (SEQ ID NO: 2800)
I076E08	1863	133 - 243	157 - 167	183 - 189	222 - 232	1 - 117	26 - 35	50 - 66	99 - 106	DQGRYDL (SEQ ID NO: 2175)
I076F06	1864	133 - 245	156 - 169	185 - 191	224 - 234	1 - 117	26 - 36	51 - 66	99 - 106	RDVQGAPY (SEQ ID NO: 3088)

I076G01	1865	143 - 254	166 - 178	194 - 200	233 - 243	1 - 127	26 - 35	50 - 66	99 - 116	VEGVYDILTGYSFADFID (SEQ ID NO: 3078)
I076H01	1866	144 - 254	168 - 178	194 - 200	233 - 243	1 - 128	26 - 35	50 - 66	99 - 117	EQGYDILTGYPGGWFDPD (SEQ ID NO: 2834)
I076H03	1867	140 - 250	164 - 174	190 - 196	229 - 239	1 - 124	26 - 34	49 - 65	98 - 113	ELGSIVGATTGALDM (SEQ ID NO: 2174)
I077B05	1868	147 - 257	169 - 182	198 - 204	237 - 246	1 - 131	26 - 37	52 - 69	102 - 120	DKSYDILTGYYYYGMDV (SEQ ID NO: 3052)
I077C10	1869	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	MEYDILTGYYGGYFDY (SEQ ID NO: 2179)
I077D01	1870	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	MEYDILTGYYGGYFDY (SEQ ID NO: 2179)
I077D04	1871	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	MEYDILTGYYGGYFDY (SEQ ID NO: 2179)
I077D11	1872	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	MEYDILTGYYGGYFDY (SEQ ID NO: 2179)
I077D12	1873	140 - 247	161 - 171	187 - 193	226 - 236	1 - 124	26 - 35	50 - 66	99 - 113	EKYDILTGYYDAFDI (SEQ ID NO: 3046)
I077E01	1874	142 - 252	164 - 177	193 - 199	232 - 241	1 - 126	26 - 35	50 - 66	99 - 115	EMGYDILTGYYLNYMDV (SEQ ID NO: 2862)
I077E03	1875	142 - 252	164 - 177	193 - 199	232 - 241	1 - 126	26 - 35	50 - 66	99 - 115	EMGYDILTGYYLNYMDV (SEQ ID NO: 2862)
I077E08	1876	141 - 248	164 - 174	190 - 196	229 - 237	1 - 125	26 - 35	50 - 66	99 - 114	MEYDILTGYYGGYFDY (SEQ ID NO: 2179)
I077F05	1877	141 - 248	162 - 172	188 - 194	227 - 237	1 - 125	26 - 35	50 - 66	99 - 114	MEYDILTGYYGGYFDY (SEQ ID NO: 2179)
I077G06	1878	141 - 251	163 - 176	192 - 198	231 - 240	1 - 125	26 - 35	50 - 66	99 - 114	MEYDILTGYYGGYFDY (SEQ ID NO: 2179)
I077H02	1879	141 - 248	164 - 174	190 - 196	229 - 237	1 - 125	26 - 35	50 - 66	99 - 114	MEYDILTGYYGGYFDY (SEQ ID NO: 2179)
I078B05	1880	143 - 253	165 - 178	194 - 200	233 - 242	1 - 127	26 - 35	50 - 66	99 - 116	ESHYDILTGYYNPSFDI (SEQ ID NO: 2994)
I079E02	1881	137 - 244	160 - 170	186 - 192	225 - 233	1 - 121	26 - 35	50 - 66	99 - 110	DSGSYYDAFDI (SEQ ID NO: 2194)
I079F11	1882	132 - 239	155 - 165	181 - 187	220 - 228	1 - 116	26 - 35	50 - 66	99 - 105	TGSGFDY (SEQ ID NO: 2192)
I082G02	1883	136 - 243	159 - 169	185 - 191	224 - 232	1 - 120	26 - 35	50 - 66	99 - 109	DGYRTNDALDI (SEQ ID NO: 2191)
I082H08	1884	131 - 242	154 - 167	183 - 189	222 - 231	1 - 115	26 - 35	50 - 66	99 - 104	DWDMDV (SEQ ID NO: 2193)
I099D03	1885	136 - 247	159 - 172	188 - 194	227 - 236	1 - 120	26 - 35	50 - 66	99 - 109	DNGGGTIGFDY (SEQ ID NO: 2195)
I079B05	1886	130 - 240	152 - 165	181 - 187	220 - 229	1 - 114	26 - 35	50 - 66	99 - 103	FVLDY (SEQ ID NO: 2210)
I079B12	1887	134 - 241	157 - 167	183 - 189	222 - 230	1 - 118	26 - 35	50 - 66	99 - 107	WTSSGAFDI (SEQ ID NO: 2205)
I079C01	1888	131 - 241	153 - 166	182 - 188	221 - 230	1 - 115	26 - 35	50 - 66	99 - 104	DWDMDV (SEQ ID NO: 2193)
I079F06	1889	134 - 241	157 - 167	183 - 189	222 - 230	1 - 118	26 - 35	50 - 66	99 - 107	DNLHAAFDI (SEQ ID NO: 2202)
I079F08	1890	138 - 248	160 - 172	188 - 194	227 - 237	1 - 122	26 - 35	50 - 66	99 - 111	YYYHSSGSADFID (SEQ ID NO: 2206)
I080A03	1891	138 - 249	161 - 173	189 - 195	228 - 238	1 - 122	26 - 35	50 - 66	99 - 111	VGIKAAAVDNFEY (SEQ ID NO: 2197)
I080A08	1892	135 - 247	158 - 171	187 - 193	226 - 236	1 - 119	26 - 35	50 - 66	99 - 108	VHSTGYAFEN (SEQ ID NO: 2200)
I080B01	1893	142 - 254	166 - 178	194 - 200	233 - 243	1 - 126	26 - 35	50 - 66	99 - 115	EYSGYHYVEGGSYAMDV (SEQ ID NO: 2201)
I080D03	1894	138 - 249	161 - 173	189 - 195	228 - 238	1 - 122	26 - 35	50 - 66	99 - 111	VGIKAAAVDNFEY (SEQ ID NO: 2197)
I080E05	1895	141 - 253	164 - 177	193 - 199	232 - 242	1 - 125	26 - 35	50 - 66	99 - 114	EGGGDAYDVAPYYFDY (SEQ ID NO: 2204)
I080G07	1896	136 - 245	161 - 172	188 - 194	227 - 234	1 - 120	26 - 35	50 - 66	99 - 109	EGPGYYGMDV (SEQ ID NO: 2209)
I080G09	1897	136 - 249	159 - 172	188 - 194	227 - 238	1 - 120	26 - 35	50 - 66	99 - 109	DNGGGTIGFDY (SEQ ID NO: 2195)
I082A05	1898	131 - 240	153 - 165	181 - 187	220 - 229	1 - 115	26 - 35	50 - 66	99 - 104	DLDFDY (SEQ ID NO: 2208)
I082B08	1899	137 - 247	159 - 171	187 - 193	226 - 236	1 - 121	26 - 35	50 - 66	99 - 110	DLGIAGTIFYDY (SEQ ID NO: 2207)
I082C03	1900	138 - 245	161 - 171	187 - 193	226 - 234	1 - 122	26 - 35	50 - 66	99 - 111	DASRDIVVLPALAI (SEQ ID NO: 2198)

I082D07	1901	134 - 241	157 - 167	183 - 189	222 - 230	1 - 118	26 - 35	50 - 66	99 - 107	WTSSGAFDI (SEQ ID NO: 2205)
I082G01	1902	138 - 245	161 - 171	187 - 193	226 - 234	1 - 122	26 - 35	50 - 66	99 - 111	DRSGWPNWYFDL (SEQ ID NO: 2212)
I083B12	1903	137 - 247	161 - 171	187 - 193	226 - 236	1 - 121	26 - 35	50 - 66	99 - 110	ESGAGGYDDY (SEQ ID NO: 2196)
I083G03	1904	138 - 249	161 - 173	189 - 195	228 - 238	1 - 122	26 - 35	50 - 66	99 - 111	VGKAAAVDNFEY (SEQ ID NO: 2197)
I084A01	1905	130 - 240	152 - 164	180 - 186	219 - 229	1 - 114	26 - 35	50 - 66	99 - 103	DTTDY (SEQ ID NO: 2203)
I084B02	1906	130 - 237	153 - 163	179 - 185	218 - 226	1 - 114	26 - 35	50 - 66	99 - 103	DTTDY (SEQ ID NO: 2203)
I084C04	1907	131 - 238	152 - 162	178 - 184	217 - 227	1 - 115	25 - 34	49 - 65	98 - 104	NLWGLDY (SEQ ID NO: 2199)
I084C11	1908	134 - 244	156 - 169	185 - 191	224 - 233	1 - 118	26 - 35	50 - 66	99 - 107	GNAWGAFDI (SEQ ID NO: 2211)
I079A01	1909	134 - 243	156 - 168	184 - 190	223 - 232	1 - 118	26 - 35	50 - 66	99 - 107	EGVAAGEDY (SEQ ID NO: 3123)
I079A03	1910	134 - 244	156 - 169	185 - 191	224 - 233	1 - 118	26 - 35	50 - 66	99 - 107	GGMDWDFDY (SEQ ID NO: 3183)
I079A04	1911	134 - 241	155 - 165	181 - 187	220 - 230	1 - 118	26 - 35	50 - 66	99 - 107	VDSSGYAYY (SEQ ID NO: 3213)
I079A06	1912	133 - 240	154 - 164	180 - 186	219 - 229	1 - 117	26 - 35	50 - 66	99 - 106	DAAVTAEG (SEQ ID NO: 3142)
I079A07	1913	136 - 246	158 - 170	186 - 192	225 - 235	1 - 120	26 - 35	50 - 66	99 - 109	GSNYSPPDAFDI (SEQ ID NO: 3112)
I079A10	1914	148 - 255	169 - 179	195 - 201	234 - 244	1 - 132	26 - 35	50 - 68	101 - 121	LPPDLRYCDGGICPGFDWLGP (SEQ ID NO: 3163)
I079A11	1915	135 - 242	158 - 168	184 - 190	223 - 231	1 - 119	26 - 35	50 - 66	99 - 108	GPSYYIMAV (SEQ ID NO: 3114)
I079B02	1916	134 - 243	156 - 168	184 - 190	223 - 232	1 - 118	26 - 35	50 - 66	99 - 107	EGVAAGEDY (SEQ ID NO: 3123)
I079B03	1917	136 - 246	158 - 170	186 - 192	225 - 235	1 - 120	26 - 35	50 - 66	99 - 109	GSNYSPPDAFDI (SEQ ID NO: 3112)
I079B04	1918	130 - 240	152 - 165	181 - 187	220 - 229	1 - 114	26 - 35	50 - 66	99 - 103	LLSDY (SEQ ID NO: 3168)
I079B07	1919	138 - 245	159 - 169	185 - 191	224 - 234	1 - 122	26 - 35	50 - 66	99 - 111	DLSGYFSRYFDY (SEQ ID NO: 3193)
I079B09	1920	139 - 246	162 - 172	188 - 194	227 - 235	1 - 123	26 - 35	50 - 66	99 - 112	VEWEDIVVGSADF (SEQ ID NO: 3128)
I079C02	1921	144 - 251	167 - 177	193 - 199	232 - 240	1 - 128	26 - 35	50 - 66	99 - 117	VTSLYSSSSGGYYGYGMDV (SEQ ID NO: 3145)
I079C04	1922	132 - 239	155 - 165	181 - 187	220 - 228	1 - 116	26 - 35	50 - 66	99 - 105	GWRGVYD (SEQ ID NO: 3195)
I079C05	1923	140 - 247	163 - 173	189 - 195	228 - 236	1 - 124	26 - 35	50 - 66	99 - 113	AGGNPRSGSLVYFDY (SEQ ID NO: 3225)
I079C07	1924	137 - 244	158 - 168	184 - 190	223 - 233	1 - 121	26 - 35	50 - 66	99 - 110	GLDVYAIYGLDV (SEQ ID NO: 3176)
I079D01	1925	144 - 254	166 - 179	195 - 201	234 - 243	1 - 128	26 - 35	50 - 66	99 - 117	EVARNYDLLTRSYLAGPLDN (SEQ ID NO: 2751)
I079D02	1926	135 - 245	157 - 169	185 - 191	224 - 234	1 - 119	26 - 35	50 - 66	99 - 108	EIGWEGAFDI (SEQ ID NO: 3178)
I079D04	1927	133 - 243	155 - 167	183 - 189	222 - 232	1 - 117	26 - 35	50 - 66	99 - 106	VRPGLMDV (SEQ ID NO: 3132)
I079D06	1928	137 - 247	159 - 171	187 - 193	226 - 236	1 - 121	26 - 35	50 - 66	99 - 110	EAYTSSWAEFDF (SEQ ID NO: 3190)
I079D07	1929	136 - 243	157 - 167	183 - 189	222 - 232	1 - 120	26 - 35	50 - 66	99 - 109	NITPLAMVGDF (SEQ ID NO: 3146)
I079D08	1930	130 - 240	152 - 165	181 - 187	220 - 229	1 - 114	26 - 35	50 - 66	99 - 103	LIEDF (SEQ ID NO: 3161)
I079D09	1931	131 - 238	152 - 162	178 - 184	217 - 227	1 - 115	26 - 35	50 - 66	99 - 104	DSGSPD (SEQ ID NO: 3108)
I079D11	1932	134 - 241	157 - 167	183 - 189	222 - 230	1 - 118	26 - 35	50 - 66	99 - 107	EGVAAGEDY (SEQ ID NO: 3123)
I079E06	1933	136 - 244	158 - 168	184 - 190	223 - 233	1 - 120	26 - 35	50 - 66	99 - 109	EKRGSRRVFDI (SEQ ID NO: 3093)
I079E08	1934	137 - 247	159 - 171	187 - 193	226 - 236	1 - 121	26 - 35	50 - 66	99 - 110	EAYASSWAEFDF (SEQ ID NO: 3189)
I079E11	1935	136 - 243	159 - 169	185 - 191	224 - 232	1 - 120	26 - 35	50 - 66	99 - 109	PYGSGYAFDI (SEQ ID NO: 3185)
I079E12	1936	143 - 253	165 - 177	193 - 199	232 - 242	1 - 127	26 - 35	50 - 66	99 - 116	ARDYYDSSGGYVPDAFDI (SEQ ID NO: 3107)

I079F01	1937	133 - 241	154 - 164	180 - 186	219 - 230	1 - 117	26 - 35	50 - 66	99 - 106	GHFYGMVDV (SEQ ID NO: 3098)
I079F02	1938	148 - 253	169 - 179	195 - 201	234 - 242	1 - 132	26 - 35	50 - 68	101 - 121	LPPDLRYCDGCMSCGFDWLGP (SEQ ID NO: 3219)
I079F03	1939	140 - 247	161 - 171	187 - 193	226 - 236	1 - 124	26 - 35	50 - 66	99 - 113	ESLLTEEYCGSDCYS (SEQ ID NO: 3115)
I079F04	1940	136 - 243	157 - 167	183 - 189	222 - 232	1 - 120	26 - 35	50 - 66	99 - 109	NSAPPAPSMVDV (SEQ ID NO: 3099)
I079F09	1941	130 - 237	151 - 161	177 - 183	216 - 226	1 - 114	26 - 35	50 - 66	99 - 103	RYDYD (SEQ ID NO: 3139)
I079F10	1942	136 - 243	157 - 167	183 - 189	222 - 232	1 - 120	26 - 35	50 - 66	99 - 109	NITPLAMVGDF (SEQ ID NO: 3146)
I079F12	1943	136 - 243	159 - 169	185 - 191	224 - 232	1 - 120	26 - 35	50 - 66	99 - 109	ADYSNDYYMDV (SEQ ID NO: 3166)
I079G02	1944	136 - 243	157 - 167	183 - 189	222 - 232	1 - 120	26 - 35	50 - 66	99 - 109	NITPLAMVGDF (SEQ ID NO: 3146)
I079G05	1945	136 - 243	159 - 169	185 - 191	224 - 232	1 - 120	26 - 35	50 - 66	99 - 109	FPLESYYYMDV (SEQ ID NO: 3124)
I079G06	1946	135 - 245	157 - 170	186 - 192	225 - 234	1 - 119	26 - 35	50 - 66	99 - 108	GNSFGRITLDY (SEQ ID NO: 3158)
I079H05	1947	136 - 243	157 - 167	183 - 189	222 - 232	1 - 120	26 - 35	50 - 66	99 - 109	DVPPPDGYLEV (SEQ ID NO: 3192)
I079H06	1948	134 - 241	157 - 167	183 - 189	222 - 230	1 - 118	26 - 35	50 - 66	99 - 107	ASYPVPFDY (SEQ ID NO: 3171)
I080A01	1949	131 - 242	154 - 166	182 - 188	221 - 231	1 - 115	26 - 35	50 - 66	99 - 104	GGWLDD (SEQ ID NO: 3210)
I080A02	1950	133 - 245	156 - 169	185 - 191	224 - 234	1 - 117	26 - 35	50 - 66	99 - 106	EHSSFDY (SEQ ID NO: 3111)
I080A05	1951	141 - 253	164 - 177	193 - 199	232 - 242	1 - 125	26 - 35	50 - 66	99 - 114	EGEGDGYNVAPYYFDY (SEQ ID NO: 3160)
I080A06	1952	141 - 250	166 - 176	192 - 198	231 - 239	1 - 125	26 - 35	50 - 66	99 - 114	EAGSGSYHFSFPFDY (SEQ ID NO: 3188)
I080A07	1953	135 - 247	158 - 171	187 - 193	226 - 236	1 - 119	26 - 35	50 - 66	99 - 108	TGIWGYFDY (SEQ ID NO: 3175)
I080A10	1954	141 - 252	164 - 176	192 - 198	231 - 241	1 - 125	26 - 35	50 - 66	99 - 114	DGNLNYDGSTDYGMDV (SEQ ID NO: 3140)
I080B02	1955	138 - 248	162 - 172	188 - 194	227 - 237	1 - 122	26 - 35	50 - 66	99 - 111	LGRNVTSSWSLDY (SEQ ID NO: 3181)
I080B03	1956	138 - 249	161 - 173	189 - 195	228 - 238	1 - 122	26 - 35	50 - 66	99 - 111	VVGYSSTLGTDV (SEQ ID NO: 3096)
I080B05	1957	137 - 249	161 - 173	189 - 195	228 - 238	1 - 121	26 - 35	50 - 66	99 - 110	LGVARGREAFDL (SEQ ID NO: 3206)
I080B06	1958	142 - 254	165 - 177	193 - 199	232 - 243	1 - 126	26 - 37	52 - 69	102 - 115	AVRSPGYYYMDV (SEQ ID NO: 3125)
I080B07	1959	133 - 243	157 - 167	183 - 189	222 - 232	1 - 117	26 - 35	50 - 66	99 - 106	GRKPLFDY (SEQ ID NO: 3141)
I080B08	1960	136 - 248	159 - 172	188 - 194	227 - 237	1 - 120	26 - 37	52 - 67	100 - 109	KQRREKYFDY (SEQ ID NO: 3100)
I080B09	1961	142 - 254	165 - 178	194 - 200	233 - 243	1 - 126	26 - 35	50 - 66	99 - 115	EKAIIETTSGEADPFDI (SEQ ID NO: 3151)
I080B10	1962	138 - 249	161 - 173	189 - 195	228 - 238	1 - 122	26 - 37	52 - 67	100 - 111	RPALRSLWYFDL (SEQ ID NO: 3102)
I080B11	1963	137 - 248	160 - 172	188 - 194	227 - 237	1 - 121	26 - 35	50 - 68	101 - 110	LHCTGGSCGF (SEQ ID NO: 3186)
I080B12	1964	139 - 253	164 - 179	195 - 201	234 - 242	1 - 123	26 - 35	50 - 66	99 - 112	NPYYIDSSEGFYD (SEQ ID NO: 3109)
I080C03	1965	138 - 248	162 - 172	188 - 194	227 - 237	1 - 122	26 - 35	50 - 66	99 - 111	SGRQAYYYGMDV (SEQ ID NO: 3091)
I080C06	1966	144 - 254	168 - 178	194 - 200	233 - 243	1 - 128	26 - 36	51 - 66	99 - 117	DYYDGSSYSSGDYYYYMDV (SEQ ID NO: 3227)
I080C07	1967	144 - 256	167 - 180	196 - 202	235 - 245	1 - 128	26 - 35	50 - 66	99 - 117	DSDLVVPTAIQGRYYFDN (SEQ ID NO: 3113)
I080C08	1968	137 - 249	160 - 173	189 - 195	228 - 238	1 - 121	26 - 35	50 - 66	99 - 110	GKRYSGWYFDI (SEQ ID NO: 3130)
I080C10	1969	131 - 243	154 - 167	183 - 189	222 - 232	1 - 115	26 - 35	50 - 66	99 - 104	DTPLDP (SEQ ID NO: 3094)
I080C11	1970	137 - 249	160 - 173	189 - 195	228 - 238	1 - 121	26 - 35	50 - 66	99 - 110	EGDPTDNDADFV (SEQ ID NO: 3155)
I080C12	1971	138 - 249	161 - 173	189 - 195	228 - 238	1 - 122	26 - 35	50 - 66	99 - 111	DGPTYARPYLDH (SEQ ID NO: 3153)
I080D01	1972	136 - 245	161 - 171	187 - 193	226 - 234	1 - 120	26 - 35	50 - 66	99 - 109	DGTYKVDWGFYD (SEQ ID NO: 3220)

Gly Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser
 195 200 205

Glu Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
 210 215 220

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr
 225 230 235 240

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
 245 250

<210> 80

<211> 250

<212> PRT

<213> Homo sapiens

<400> 80

Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His
 20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
 35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Pro Phe Tyr Asp Thr Leu Thr Ser Tyr Val Gly Pro Tyr Gly
 100 105 110

Thr Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly
 115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr Thr
 130 135 140

Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
145 150 155 160

Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val Ala
165 170 175

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr Gly
180 185 190

Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser Lys
195 200 205

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp
210 215 220

Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr Phe
225 230 235 240

Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
245 250

<210> 81
<211> 250
<212> PRT
<213> Homo sapiens

<400> 81
Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Pro Phe Tyr Asp Thr Leu Thr Ser Tyr Val Thr Thr Pro Cys

100 105 110
 Thr Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly
 115 120 125
 Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr Thr
 130 135 140
 Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
 145 150 155 160
 Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val Ala
 165 170 175
 Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr Gly
 180 185 190
 Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser Glu
 195 200 205
 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp
 210 215 220
 Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr Phe
 225 230 235 240
 Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
 245 250

<210> 82
 <211> 244
 <212> PRT
 <213> Homo sapiens

<400> 82
 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Asp Trp Val
 35 40 45

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val
 50 55 60

Glu Gly Arg Phe Ala Val Ser Arg Asp Asn Ala Lys Asn Ala Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Thr Lys Ala Ser Tyr Leu Ser Thr Ser Ser Ser Leu Asp Asn Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
130 135 140

Ser Ser Leu Ser Ala Ser Ile Gly Asp Arg Val Thr Ile Thr Cys Arg
145 150 155 160

Ala Ser Gln Gly Ile Arg Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser
180 185 190

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys
210 215 220

Gln Lys Tyr Asn Ser Ala Pro Tyr Ala Phe Gly Gln Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Arg

<210> 83

<211> 251

<212> PRT

<213> Homo sapiens

<400> 83

Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asp His
 20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
 35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Pro Phe Tyr Asp Thr Leu Thr Ser Tyr Val Phe Gln Tyr Phe
 100 105 110

Asp His Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr
 130 135 140

Thr Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Glu Arg
 145 150 155 160

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val
 165 170 175

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr
 180 185 190

Gly Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser
 195 200 205

Glu Thr Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
 210 215 220

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr
 225 230 235 240

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
 245 250

<210> 84
 <211> 251
 <212> PRT
 <213> Homo sapiens

<400> 84
 Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His
 20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
 35 40 45

Gly Trp Ile Ser Gly His Gly Asp Ser Thr Lys Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Pro Phe Tyr Asp Thr Leu Thr Ser Tyr Val Ile Pro Phe Leu
 100 105 110

Pro Leu Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr
 130 135 140

Thr Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Glu Arg
 145 150 155 160

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val
 165 170 175

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr
 180 185 190

Gly Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser
 195 200 205

Glu Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
210 215 220

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr
225 230 235 240

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
245 250

<210> 85
<211> 251
<212> PRT
<213> Homo sapiens

<400> 85
Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Pro Phe Tyr Asp Thr Leu Thr Ser Tyr Val Leu His Ile Tyr
100 105 110

Pro His Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr
130 135 140

Thr Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Glu Arg
145 150 155 160

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val
165 170 175

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr
180 185 190

Gly Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
210 215 220

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr
225 230 235 240

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
245 250

<210> 86

<211> 251

<212> PRT

<213> Homo sapiens

<400> 86

Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Val Ser Gly Tyr Thr Phe Ser Asn His
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Pro Phe Tyr Asp Thr Leu Thr Asn Tyr Val Phe Glu Tyr Tyr
100 105 110

Ala Ser Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly

115 120 125

115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr
130 135 140

Thr Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Glu Arg
145 150 155 160

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val
165 170 175

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr
180 185 190

Gly Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

Glu Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
210 215 220

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr
225 230 235 240

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
245 250

<210> 87
<211> 251
<212> PRT
<213> Homo sapiens

<400> 87
Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Pro Phe Tyr Asp Thr Leu Thr Ser Tyr Val Ile Leu Tyr Tyr
100 105 110

Leu His Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr
130 135 140

Thr Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Glu Arg
145 150 155 160

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val
165 170 175

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr
180 185 190

Gly Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

Glu Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
210 215 220

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr
225 230 235 240

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
245 250

<210> 88

<211> 251

<212> PRT

<213> Homo sapiens

<400> 88

Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
 35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Pro Phe Tyr Asp Thr Leu Thr Ser Tyr Val Phe Gln Tyr Phe
 100 105 110

Asp His Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr
 130 135 140

Thr Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Glu Arg
 145 150 155 160

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val
 165 170 175

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr
 180 185 190

Gly Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser
 195 200 205

Glu Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
 210 215 220

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Pro Thr
 225 230 235 240

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
 245 250

<210> 89

<211> 251

<212> PRT

<213> Homo sapiens

<400> 89

Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Pro Phe Tyr Asp Thr Leu Thr Ser Tyr Val Leu Met Tyr Phe
100 105 110

Pro His Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr
130 135 140

Thr Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Glu Arg
145 150 155 160

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val
165 170 175

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr
180 185 190

Gly Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

Glu Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
210 215 220

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr
 225 230 235 240

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
 245 250

<210> 90
 <211> 251
 <212> PRT
 <213> Homo sapiens

<400> 90
 Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His
 20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
 35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Pro Phe Tyr Asp Thr Leu Thr Ser Tyr Val Leu Phe Phe Tyr
 100 105 110

Pro Leu Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr
 130 135 140

Thr Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Glu Arg
 145 150 155 160

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val
 165 170 175

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr
180 185 190

Gly Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

Glu Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
210 215 220

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr
225 230 235 240

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
245 250

<210> 91

<211> 251

<212> PRT

<213> Homo sapiens

<400> 91

Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Pro Phe Tyr Asp Thr Leu Thr Ser Tyr Val Phe Gln Tyr Phe
100 105 110

Asp His Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr

634433: 640330

Ala Arg Pro Phe Tyr Asp Thr Leu Thr Ser Tyr Val Phe Asp Tyr Tyr
 100 105 110

Ala Ser Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr
 130 135 140

Thr Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Glu Arg
 145 150 155 160

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val
 165 170 175

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr
 180 185 190

Gly Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser
 195 200 205

Glu Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
 210 215 220

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr
 225 230 235 240

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
 245 250

<210> 93

<211> 251

<212> PRT

<213> Homo sapiens

<400> 93

Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His
 20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
 35 40 45

Gly Trp Ile Ser Gly His Gly Asp Ser Thr Lys Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Pro Phe Tyr Asp Thr Leu Thr Ser Tyr Val Ile Pro Phe Leu
100 105 110

Pro Leu Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr
130 135 140

Thr Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Glu Arg
145 150 155 160

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val
165 170 175

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr
180 185 190

Gly Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

Glu Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
210 215 220

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr
225 230 235 240

Phe Gly Gln Gly Thr Arg Leu Glu Ile Ser Arg
245 250

<210> 94

<211> 251

<212> PRT

<213> Homo sapiens

<400> 94

Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asn His
20 25 30

Ser Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
35 40 45

Gly Trp Ile Ser Gly His Asp Asp Ser Thr Lys Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Ile Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Pro Phe Tyr Asp Thr Leu Thr Ser Tyr Val Phe Gln Tyr Phe
100 105 110

Asp His Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Glu Thr
130 135 140

Thr Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Glu Arg
145 150 155 160

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Arg Gly Trp Val
165 170 175

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met Tyr
180 185 190

Gly Thr Ser Arg Arg Ala Thr Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

Glu Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
210 215 220

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Thr Ser Pro Arg Thr
225 230 235 240

I081A10	2009	133 - 243	155 - 168	184 - 190	223 - 232	1 - 117	26 - 35	50 - 66	99 - 106	GGDRAFDI (SEQ ID NO: 3119)
I081B01	2010	130 - 236	151 - 161	177 - 183	216 - 225	1 - 114	26 - 35	50 - 66	99 - 103	DTTDY (SEQ ID NO: 2203)
I081B04	2011	134 - 244	156 - 169	185 - 191	224 - 233	1 - 118	26 - 35	50 - 66	99 - 107	GNAWGAFDI (SEQ ID NO: 2211)
I081B05	2012	133 - 243	155 - 168	184 - 190	223 - 232	1 - 117	26 - 35	50 - 66	99 - 106	GGDRAFDI (SEQ ID NO: 3119)
I081B06	2013	133 - 240	154 - 164	180 - 186	219 - 229	1 - 117	26 - 35	50 - 66	99 - 106	VKRYFDY (SEQ ID NO: 3179)
I081B07	2014	136 - 243	157 - 167	183 - 189	222 - 232	1 - 120	26 - 35	50 - 66	99 - 109	ELTGANDAFDI (SEQ ID NO: 3104)
I081B08	2015	132 - 239	153 - 163	179 - 185	218 - 228	1 - 116	26 - 35	50 - 66	99 - 105	RRYALDY (SEQ ID NO: 2920)
I081B09	2016	130 - 240	152 - 164	180 - 186	219 - 229	1 - 114	26 - 35	50 - 66	99 - 103	DTTDY (SEQ ID NO: 2203)
I081B10	2017	130 - 237	153 - 163	179 - 185	218 - 226	1 - 114	26 - 35	50 - 66	99 - 103	DTTDY (SEQ ID NO: 2203)
I081B11	2018	132 - 239	153 - 163	179 - 185	218 - 228	1 - 116	26 - 35	50 - 66	99 - 105	GFALYKD (SEQ ID NO: 3169)
I081C07	2019	130 - 237	153 - 163	179 - 185	218 - 226	1 - 114	26 - 35	50 - 66	99 - 103	DTTDY (SEQ ID NO: 2203)
I081C08	2020	130 - 237	153 - 163	179 - 185	218 - 226	1 - 114	26 - 35	50 - 66	99 - 103	DTTDY (SEQ ID NO: 2203)
I081D04	2021	135 - 242	156 - 166	182 - 188	221 - 231	1 - 119	26 - 35	50 - 66	99 - 108	EDLTGDAFDI (SEQ ID NO: 3103)
I081D06	2022	132 - 239	153 - 163	179 - 185	218 - 228	1 - 116	26 - 35	50 - 66	99 - 105	GDAYFDY (SEQ ID NO: 3147)
I081D08	2023	132 - 239	153 - 163	179 - 185	218 - 228	1 - 116	26 - 35	50 - 66	99 - 105	GDAYFDY (SEQ ID NO: 3147)
I081D09	2024	130 - 238	152 - 162	178 - 184	217 - 227	1 - 114	26 - 35	50 - 66	99 - 103	DTTDY (SEQ ID NO: 2203)
I081D10	2025	130 - 240	152 - 164	180 - 186	219 - 229	1 - 114	26 - 35	50 - 66	99 - 103	DTTDY (SEQ ID NO: 2203)
I081D11	2026	134 - 244	156 - 169	185 - 191	224 - 233	1 - 118	26 - 35	50 - 66	99 - 107	EGLLDAFDI (SEQ ID NO: 3200)
I081D12	2027	130 - 237	153 - 163	179 - 185	218 - 226	1 - 114	26 - 35	50 - 66	99 - 103	DTTDY (SEQ ID NO: 2203)
I081E02	2028	130 - 237	153 - 163	179 - 185	218 - 226	1 - 114	26 - 35	50 - 66	99 - 103	DTTDY (SEQ ID NO: 2203)
I081E03	2029	130 - 240	152 - 164	180 - 186	219 - 229	1 - 114	26 - 35	50 - 66	99 - 103	DTTDY (SEQ ID NO: 2203)
I081E05	2030	130 - 240	152 - 164	180 - 186	219 - 229	1 - 114	26 - 35	50 - 66	99 - 103	DTTDY (SEQ ID NO: 2203)
I081E06	2031	134 - 241	155 - 165	181 - 187	220 - 230	1 - 118	26 - 35	50 - 66	99 - 107	VGYGKGDY (SEQ ID NO: 3137)
I081E07	2032	134 - 241	155 - 165	181 - 187	220 - 230	1 - 118	26 - 35	50 - 66	99 - 107	GAGRYFDL (SEQ ID NO: 3118)
I081E10	2033	142 - 249	163 - 173	189 - 195	228 - 238	1 - 126	26 - 35	50 - 66	99 - 115	GLAPVDGGMNTDAFDI (SEQ ID NO: 3184)
I081F01	2034	130 - 239	152 - 164	180 - 186	219 - 228	1 - 114	26 - 35	50 - 66	99 - 103	DTTDY (SEQ ID NO: 2203)
I081F04	2035	132 - 239	153 - 163	179 - 185	218 - 228	1 - 116	26 - 35	50 - 66	99 - 105	RLRKAR (SEQ ID NO: 3170)
I081F05	2036	130 - 237	151 - 161	177 - 183	216 - 226	1 - 114	26 - 35	50 - 66	99 - 103	DTTDY (SEQ ID NO: 2203)
I081F06	2037	134 - 244	156 - 169	185 - 191	224 - 233	1 - 118	26 - 35	50 - 66	99 - 107	ERGNQAFDI (SEQ ID NO: 3156)
I081F07	2038	132 - 239	153 - 163	179 - 185	218 - 228	1 - 116	26 - 35	50 - 66	99 - 105	RRYALDY (SEQ ID NO: 2920)
I081F11	2039	130 - 237	151 - 161	177 - 183	216 - 226	1 - 114	26 - 35	50 - 66	99 - 103	DTTDY (SEQ ID NO: 2203)
I081G01	2040	130 - 237	153 - 163	179 - 185	218 - 226	1 - 114	26 - 35	50 - 66	99 - 103	DTTDY (SEQ ID NO: 2203)
I081G04	2041	130 - 240	152 - 164	180 - 186	219 - 229	1 - 114	26 - 35	50 - 66	99 - 103	DTTDY (SEQ ID NO: 2203)
I081G06	2042	135 - 245	157 - 170	186 - 192	225 - 234	1 - 119	26 - 35	50 - 66	99 - 108	SRSPYDAFDI (SEQ ID NO: 3097)
I081G10	2043	130 - 237	153 - 163	179 - 185	218 - 226	1 - 114	26 - 35	50 - 66	99 - 103	DTTDY (SEQ ID NO: 2203)
I081H02	2044	130 - 240	152 - 164	180 - 186	219 - 229	1 - 114	26 - 35	50 - 66	99 - 103	DTTDY (SEQ ID NO: 2203)

I081H03	2045	130 - 240	152 - 164	180 - 186	219 - 229	1 - 114	26 - 35	50 - 66	99 - 103	DTTDY (SEQ ID NO: 2203)
I081H04	2046	135 - 242	156 - 166	182 - 188	221 - 231	1 - 119	26 - 35	50 - 66	99 - 108	SNWGGDAFDI (SEQ ID NO: 3202)
I081H06	2047	130 - 240	152 - 165	181 - 187	220 - 229	1 - 114	26 - 35	50 - 66	99 - 103	LAFDI (SEQ ID NO: 3174)
I081H08	2048	130 - 240	152 - 164	180 - 186	219 - 229	1 - 114	26 - 35	50 - 66	99 - 103	DTTDY (SEQ ID NO: 2203)
I082A02	2049	139 - 249	161 - 173	189 - 195	228 - 238	1 - 123	26 - 35	50 - 66	99 - 112	PAASSRGPKDAFDI (SEQ ID NO: 3129)
I082A04	2050	130 - 240	152 - 165	181 - 187	220 - 229	1 - 114	26 - 35	50 - 66	99 - 103	LSGDS (SEQ ID NO: 3122)
I082A08	2051	134 - 243	156 - 168	184 - 190	223 - 232	1 - 118	26 - 35	50 - 66	99 - 107	EGVAAGEDY (SEQ ID NO: 3123)
I082A11	2052	130 - 240	152 - 165	181 - 187	220 - 229	1 - 114	26 - 35	50 - 66	99 - 103	FVLDDY (SEQ ID NO: 2210)
I082B06	2053	131 - 238	154 - 164	180 - 186	219 - 227	1 - 115	26 - 35	50 - 66	99 - 104	GNGKDV (SEQ ID NO: 3135)
I082B09	2054	134 - 241	157 - 167	183 - 189	222 - 230	1 - 118	26 - 35	50 - 66	99 - 107	EGVAAGEDY (SEQ ID NO: 3123)
I082B12	2055	131 - 241	153 - 166	182 - 188	221 - 230	1 - 115	26 - 35	50 - 66	99 - 104	DLDFDY (SEQ ID NO: 2208)
I082C01	2056	136 - 243	157 - 167	183 - 189	222 - 232	1 - 120	26 - 35	50 - 66	99 - 109	VNDIVVMDV (SEQ ID NO: 3143)
I082C05	2057	136 - 243	157 - 167	183 - 189	222 - 232	1 - 120	26 - 35	50 - 66	99 - 109	EKRGSRRVFDI (SEQ ID NO: 3093)
I082C08	2058	137 - 244	158 - 168	184 - 190	223 - 233	1 - 121	26 - 35	50 - 66	99 - 110	LSNRNDNRLDY (SEQ ID NO: 3106)
I082D02	2059	130 - 240	152 - 165	181 - 187	220 - 229	1 - 114	26 - 35	50 - 66	99 - 103	FVLDDY (SEQ ID NO: 2210)
I082E05	2060	134 - 241	155 - 165	181 - 187	220 - 230	1 - 118	26 - 35	50 - 66	99 - 107	TWATNTFDM (SEQ ID NO: 3152)
I082E06	2061	130 - 240	152 - 165	181 - 187	220 - 229	1 - 114	26 - 35	50 - 66	99 - 103	FDLDDY (SEQ ID NO: 3167)
I082E07	2062	139 - 246	162 - 172	188 - 194	227 - 235	1 - 123	26 - 35	50 - 66	99 - 112	VEWEDIVGSAFDI (SEQ ID NO: 3128)
I082F11	2063	136 - 243	159 - 169	185 - 191	224 - 232	1 - 120	26 - 35	50 - 66	99 - 109	GGDMTTVTDDY (SEQ ID NO: 3177)
I082G07	2064	136 - 243	159 - 169	185 - 191	224 - 232	1 - 120	26 - 35	50 - 66	99 - 109	ADYSNDYYMDV (SEQ ID NO: 3166)
I082G10	2065	134 - 249	160 - 173	189 - 195	228 - 238	1 - 118	26 - 35	50 - 66	99 - 107	EGVAAGEDY (SEQ ID NO: 3123)
I082G11	2066	143 - 250	164 - 174	190 - 196	229 - 239	1 - 127	26 - 35	50 - 66	99 - 116	GPIYYFDGSA YEGYYFDY (SEQ ID NO: 3223)
I082H04	2067	132 - 238	153 - 163	179 - 185	218 - 227	1 - 116	26 - 35	50 - 65	98 - 105	MNADAFEI (SEQ ID NO: 3223)
I082H09	2068	139 - 246	160 - 170	186 - 192	225 - 235	1 - 123	26 - 35	50 - 66	99 - 112	PAASSRGPKDAFDI (SEQ ID NO: 3129)
I083A06	2069	136 - 244	159 - 169	185 - 191	224 - 233	1 - 120	26 - 35	50 - 66	99 - 109	DSRPTNRAHY (SEQ ID NO: 3110)
I083A09	2070	137 - 248	160 - 172	188 - 194	227 - 237	1 - 121	26 - 35	50 - 68	101 - 110	LHCTGGSCGF (SEQ ID NO: 3186)
I083A11	2071	135 - 248	158 - 171	187 - 193	226 - 237	1 - 119	26 - 35	50 - 66	99 - 108	VRDDSAGFDY (SEQ ID NO: 3173)
I083B03	2072	137 - 247	161 - 171	187 - 193	226 - 236	1 - 121	26 - 35	50 - 66	99 - 110	VLVRGQYRGMDL (SEQ ID NO: 3138)
I083B05	2073	138 - 250	161 - 174	190 - 196	229 - 239	1 - 122	26 - 35	50 - 66	99 - 111	VDYTDYEMGAIDL (SEQ ID NO: 3172)
I083B06	2074	138 - 250	161 - 174	190 - 196	229 - 239	1 - 122	26 - 35	50 - 66	99 - 111	DRIAAGGDAFDI (SEQ ID NO: 3194)
I083B10	2075	137 - 246	162 - 172	188 - 194	227 - 235	1 - 121	26 - 35	50 - 66	99 - 110	DLKNGYALFDS (SEQ ID NO: 3197)
I083C01	2076	135 - 247	158 - 171	187 - 193	226 - 236	1 - 119	26 - 35	50 - 66	99 - 108	DEYSSLYMDV (SEQ ID NO: 3201)
I083C02	2077	135 - 246	158 - 171	187 - 193	226 - 235	1 - 119	26 - 35	50 - 66	99 - 108	FGAGRLYDDY (SEQ ID NO: 3224)
I083C07	2078	136 - 249	159 - 172	188 - 194	227 - 238	1 - 120	26 - 35	50 - 66	99 - 109	DNGGGTIGFDY (SEQ ID NO: 2195)
I083C12	2079	135 - 246	158 - 171	187 - 193	226 - 235	1 - 119	26 - 35	50 - 66	99 - 108	DQGIETANDY (SEQ ID NO: 3207)
I083D04	2080	145 - 256	168 - 181	197 - 203	236 - 245	1 - 129	26 - 35	50 - 66	99 - 118	DILPDYDFWPNEDASSLDT (SEQ ID NO: 3133)

I083D07	2081	148 - 262	173 - 188	204 - 210	243 - 251	1 - 132	26 - 35	50 - 66	99 - 121	DFQVVRGVFIANPPIYNYGMDV (SEQ ID NO: 3154)
I083D08	2082	142 - 254	165 - 178	194 - 200	233 - 243	1 - 126	26 - 35	50 - 66	99 - 115	DADEGLVEAETTNWFDS (SEQ ID NO: 3126)
I083D10	2083	146 - 258	169 - 181	197 - 203	236 - 247	1 - 130	26 - 37	52 - 69	102 - 119	ATKSYDILTRMYYYHMDV (SEQ ID NO: 2748)
I083D12	2084	132 - 242	156 - 166	182 - 188	221 - 231	1 - 116	26 - 35	50 - 66	99 - 105	DRTRMDV (SEQ ID NO: 3182)
I083E02	2085	138 - 249	161 - 173	189 - 195	228 - 238	1 - 122	26 - 35	50 - 66	99 - 111	VGIKAAAVDNFEY (SEQ ID NO: 2197)
I083E03	2086	135 - 248	158 - 171	187 - 193	226 - 237	1 - 119	26 - 35	50 - 66	99 - 108	DEYNDAFDY (SEQ ID NO: 3105)
I083E04	2087	143 - 255	166 - 179	195 - 201	234 - 244	1 - 127	26 - 35	50 - 66	99 - 116	DGDISDSPINNQNQYAMD (SEQ ID NO: 3101)
I083E08	2088	138 - 248	162 - 172	188 - 194	227 - 237	1 - 122	26 - 35	50 - 66	99 - 111	RGGTSENYSYSGMDV (SEQ ID NO: 3209)
I083E12	2089	134 - 245	157 - 170	186 - 192	225 - 234	1 - 118	26 - 35	50 - 66	99 - 107	DYPHNAFDI (SEQ ID NO: 3127)
I083F02	2090	145 - 258	168 - 181	197 - 203	236 - 247	1 - 129	26 - 35	50 - 66	99 - 118	DVRSDFWSGGYFHYSGMDV (SEQ ID NO: 3131)
I083F04	2091	137 - 248	160 - 172	188 - 194	227 - 237	1 - 121	26 - 35	50 - 66	99 - 110	STLEVGAATDFDY (SEQ ID NO: 3199)
I083F06	2092	134 - 247	157 - 170	186 - 192	225 - 236	1 - 118	26 - 35	50 - 66	99 - 107	SDDWGAYHI (SEQ ID NO: 3198)
I083F08	2093	138 - 250	161 - 174	190 - 196	229 - 239	1 - 122	26 - 35	50 - 66	99 - 111	ERGGRDGDYALDF (SEQ ID NO: 3148)
I083F11	2094	136 - 248	159 - 172	188 - 194	227 - 237	1 - 120	26 - 35	50 - 66	99 - 109	ELVGAPGGFDP (SEQ ID NO: 3191)
I083G04	2095	138 - 250	161 - 174	190 - 196	229 - 239	1 - 122	26 - 35	50 - 66	99 - 111	VDYTDYEMGAIDL (SEQ ID NO: 3172)
I083G05	2096	137 - 249	161 - 173	189 - 195	228 - 238	1 - 121	26 - 35	50 - 68	101 - 110	SVAGRGNFDY (SEQ ID NO: 3208)
I083G06	2097	138 - 250	161 - 174	190 - 196	229 - 239	1 - 122	26 - 35	50 - 66	99 - 111	ERGGRDGDYALDF (SEQ ID NO: 3148)
I083G08	2098	141 - 253	164 - 177	193 - 199	232 - 242	1 - 125	26 - 35	50 - 66	99 - 114	EGGGDAYDVAPYYFDY (SEQ ID NO: 2204)
I083G09	2099	130 - 242	154 - 166	182 - 188	221 - 231	1 - 114	26 - 35	50 - 66	99 - 103	DPFDY (SEQ ID NO: 3134)
I083G11	2100	140 - 252	163 - 176	192 - 198	231 - 241	1 - 124	26 - 35	50 - 66	99 - 113	ALLGLPSDFSYYVDV (SEQ ID NO: 3159)
I083H04	2101	141 - 253	164 - 177	193 - 199	232 - 242	1 - 125	26 - 35	50 - 66	99 - 114	EGEGDGYNVAPYYFDY (SEQ ID NO: 3160)
I083H05	2102	133 - 243	157 - 167	183 - 189	222 - 232	1 - 117	26 - 35	50 - 66	99 - 106	TDYGGFDY (SEQ ID NO: 3092)
I083H07	2103	137 - 247	161 - 171	187 - 193	226 - 236	1 - 121	26 - 35	50 - 66	99 - 110	GGVGDSRGVFD (SEQ ID NO: 3162)
I084A03	2104	130 - 237	153 - 163	179 - 185	218 - 226	1 - 114	26 - 35	50 - 66	99 - 103	DTTDY (SEQ ID NO: 2203)
I084A08	2105	130 - 240	152 - 164	180 - 186	219 - 229	1 - 114	26 - 35	50 - 66	99 - 103	DTTDY (SEQ ID NO: 2203)
I084B08	2106	135 - 242	156 - 166	182 - 188	221 - 231	1 - 119	26 - 35	50 - 66	99 - 108	ESLTGDAFDI (SEQ ID NO: 3116)
I084C02	2107	136 - 243	157 - 167	183 - 189	222 - 232	1 - 120	26 - 35	50 - 66	99 - 109	SPLHFSDAFDI (SEQ ID NO: 3120)
I084D03	2108	130 - 240	152 - 164	180 - 186	219 - 229	1 - 114	26 - 35	50 - 66	99 - 103	DTTDY (SEQ ID NO: 2203)
I084D05	2109	133 - 243	155 - 168	184 - 190	223 - 232	1 - 117	26 - 35	50 - 66	99 - 106	EVGGAFDI (SEQ ID NO: 3157)
I084E01	2110	130 - 237	153 - 163	179 - 185	218 - 226	1 - 114	26 - 35	50 - 66	99 - 103	DTTDY (SEQ ID NO: 2203)
I084E06	2111	130 - 237	153 - 163	179 - 185	218 - 226	1 - 114	26 - 35	50 - 66	99 - 103	DTTDY (SEQ ID NO: 2203)
I084E10	2112	130 - 237	151 - 161	177 - 183	216 - 226	1 - 114	26 - 35	50 - 66	99 - 103	DTTDY (SEQ ID NO: 2203)
I084E12	2113	130 - 240	152 - 164	180 - 186	219 - 229	1 - 114	26 - 35	50 - 66	99 - 103	DTTDY (SEQ ID NO: 2203)
I084F04	2114	130 - 237	153 - 163	179 - 185	218 - 226	1 - 114	26 - 35	50 - 66	99 - 103	DTTDY (SEQ ID NO: 2203)
I084F07	2115	130 - 237	153 - 163	179 - 185	218 - 226	1 - 114	26 - 35	50 - 66	99 - 103	DTTDY (SEQ ID NO: 2203)
I084F12	2116	135 - 245	157 - 170	186 - 192	225 - 234	1 - 119	26 - 35	50 - 66	99 - 108	ESLTGDAFDI (SEQ ID NO: 3116)

